

Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser			
100	105	110	
cgg aac gtg gca tgt gat gat ccg tcc tcg ctc gat ttc ctg agg aag			384
Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys			
115	120	125	
att caa gag cgt tca ggt cta ggt gat gag acg tac agt cct gag gga			432
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly			
130	135	140	
ctc att cac gta cca ccg cgg aag act ttt gca gcg tca cgt gaa gag			480
Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu			
145	150	155	160
aca gag aag gtt atc atc ggt gcg ctc gaa aat cta ttc gag aac acc			528
Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Glu Asn Thr			
165	170	175	
aaa gtt aac cct aga gag att ggt ata ctt gtg gtg aac tca agc atg			576
Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met			
180	185	190	
ttt aat cca act cct tcg cta tcc gct atg gtc gtt aat act ttc aag			624
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys			
195	200	205	
ctc cga agc aac atc aaa agc ttt aat cta gga gga atg ggt tgt agt			672
Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser			
210	215	220	
gct ggt gtt att gcc att gat ttg gct aaa gac ttg ttg cat gtt cat			720
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His			
225	230	235	240
aaa aac act tat gct ctt gtg gtg agc act gag aac atc aca caa ggc			768
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Gly			
245	250	255	
att tat gct gga gaa aat aga tca atg atg gtt agc aat tgc ttg ttt			816
Ile Tyr Ala Gly Glu Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe			
260	265	270	
cgt gtt ggt ggg gcc gcg att ttg ctc tct aac aag tcg gga gac cgg			864
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Ser Gly Asp Arg			
275	280	285	
aga cgg tcc aag tac aag cta gtt cac acg gtc cga acg cat act gga			912
Arg Arg Ser Lys Tyr Lys Leu Val His Thr Val Arg Thr His Thr Gly			
290	295	300	
gct gat gac aag tct ttt cga tgt gtg caa caa gaa gac gat gag agc			960
Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Glu Asp Asp Glu Ser			
305	310	315	320
ggc aaa atc gga gtt tgt ctg tca aag gac ata acc aat gtt gcg ggg			1008

Gly Lys Ile Gly Val Cys Leu Ser Lys Asp Ile Thr Asn Val Ala Gly			
325	330	335	
aca aca ctt acg aaa aat ata gca aca ttg ggt ccg ttg att ctt cct			1056
Thr Thr Leu Thr Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro			
340	345	350	
tta agc gaa aag ttt ctt ttc gct acc ttc gtc gcc aag aaa ctt			1104
Leu Ser Glu Lys Phe Leu Phe Phe Ala Thr Phe Val Ala Lys Lys Leu			
355	360	365	
cta aag gat aaa atc aag cat tac tat gtt ccg gat ttc aag ctt gct			1152
Leu Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala			
370	375	380	
gtt gac cat ttc tgt att cat gcc gga ggc aga gcc gtg atc gat gag			1200
Val Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu			
385	390	395	400
cta gag aag aac tta gga cta tcg ccg atc gat gtg gag gca tct aga			1248
Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg			
405	410	415	
tca acg tta cat aga ttt ggg aat act tca tct agc tca att tgg tat			1296
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr			
420	425	430	
gaa tta gca tac ata gag gca aag gga aga atg aag aaa ggg aat aaa			1344
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys			
435	440	445	
gct tgg cag att gct tta gga tca ggg ttt aag tgt aat agt gcg gtt			1392
Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val			
450	455	460	
tgg gtg gct cta cgc aat gtc aag gca tcg gca aat agt cct tgg caa			1440
Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln			
465	470	475	480
cat tgc atc gat aga tat ccg gtt aaa att gat tct gat ttg tca aag			1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys			
485	490	495	
tca aag act cat gtc caa aac ggt cggtcc taatttgatg tatctgagtg			1538
Ser Lys Thr His Val Gln Asn Gly Arg Ser			
500	505		
ccaacgttta ctttgtcttt cctttctttt attgggtatg aatttagatgt ttactaatgt			1598
tcctctcttt ttcgttataa ataaagaagt tcaattcttc ctatagttc aaacgcgatt			1658
ttaagcggtt ctat taggt ttacatgaat ttctttaca aaccatcttt t			1709
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 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
 35 40 45
 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
 50 55 60
 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
 65 70 75 80
 Asp Tyr Ser Cys Tyr Leu Pro Pro His Leu Lys Val Ser Val Ser
 85 90 95
 Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser
 100 105 110
 Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys
 115 120 125
 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly
 130 135 140
 Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu
 145 150 155 160
 Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Glu Asn Thr
 165 170 175
 Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met
 180 185 190
 Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
 195 200 205
 Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Met Gly Cys Ser
 210 215 220
 Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
 225 230 235 240
 Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Gly
 245 250 255
 Ile Tyr Ala Gly Glu Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
 260 265 270
 Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Ser Gly Asp Arg
 275 280 285
 Arg Arg Ser Lys Tyr Lys Leu Val His Thr Val Arg Thr His Thr Gly
 290 295 300
 Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Glu Asp Asp Glu Ser
 305 310 315 320
 Gly Lys Ile Gly Val Cys Leu Ser Lys Asp Ile Thr Asn Val Ala Gly
 325 330 335
 Thr Thr Leu Thr Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
 340 345 350
 Leu Ser Glu Lys Phe Leu Phe Phe Ala Thr Phe Val Ala Lys Lys Leu
 355 360 365
 Leu Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
 370 375 380
 Val Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu
 385 390 395 400
 Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr
 420 425 430
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys

435	440	445
Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val		
450	455	460
Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln		
465	470	475
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys		
485	490	495
Ser Lys Thr His Val Gln Asn Gly Arg Ser		
500	505	

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<213> Brassica napus

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ctt ttc aac ctt tgc ttc ttt ccg tta acg gcg atc gtc gcc gga aaa			96
Leu Phe Asn Leu Cys Phe Pro Leu Thr Ala Ile Val Ala Gly Lys			
20	25	30	
gcc tat cgg ctt acc ata gac gat ctt cac cac tta tac tat tcc tat			144
Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr			
35	40	45	
ctc caa cac aac ctc ata acc atc gct cca ctc ttt gcc ttc acc gtt			192
Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val			
50	55	60	
ttc ggt tcg gtt ctc tac atc gca acc cgg ccc aaa ccg gtt tac ctc			240
Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu			
65	70	75	80
gtt gag tac tca tgc tac ctt cca cca acg cat tgt aga tca agt atc			288
Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile			
85	90	95	
tcc aag gtc atg gat atc ttt tat caa gta aga aaa gct gat cct tct			336
Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser			
100	105	110	
cgg aac ggc acg tgc gat gac tcg tcg tgg ctt gac ttc ttg agg aag			384
Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys			
115	120	125	
att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg			432
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly			
130	135	140	

ctg ctt cag gtc cct ccc cg ^g aag act ttt gc ^g gc ^g gc ^g cgt gaa gag	480
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu	
145 150 155 160	
acg gag caa gtt atc att ggt gc ^g cta gaa aat cta ttc aag aac acc	528
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr	
165 170 175	
aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg	576
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met	
180 185 190	
ttt aat cca act cca tcg ctc tcc gc ^g atg gc ^g ttt aac act ttc aag	624
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys	
195 200 205	
ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt	672
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser	
210 215 220	
gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat	720
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His	
225 230 235 240	
aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac	768
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn	
245 250 255	
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc	816
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe	
260 265 270	
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt	864
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg	
275 280 285	
aga cg ^g tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga	912
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly	
290 295 300	
gct gac ggc aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac	960
Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn	
305 310 315 320	
ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt	1008
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly	
325 330 335	
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg	1056
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro	
340 345 350	
tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt	1104
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu	
355 360 365	

ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct	1152
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala	
370 375 380	
att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg	1200
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val	
385 390 395 400	
cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga	1248
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg	
405 410 415	
tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat	1296
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr	
420 425 430	
gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa	1344
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys	
435 440 445	
gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt	1392
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val	
450 455 460	
tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa	1440
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu	
465 470 475 480	
cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag	1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys	
485 490 495	
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Ser Glu Thr Arg Val Gln Asn Gly Arg Ser *	
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 <213> Brassica napus

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 Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr
 35 40 45
 Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val
 50 55 60
 Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu
 65 70 75 80
 Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile
 85 90 95
 Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser

100	105	110	
Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys			
115	120	125	
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly			
130	135	140	
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu			
145	150	155	160
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr			
165	170	175	
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met			
180	185	190	
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys			
195	200	205	
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser			
210	215	220	
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His			
225	230	235	240
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn			
245	250	255	
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe			
260	265	270	
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg			
275	280	285	
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly			
290	295	300	
Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn			
305	310	315	320
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly			
325	330	335	
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro			
340	345	350	
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu			
355	360	365	
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala			
370	375	380	
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val			
385	390	395	400
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg			
405	410	415	
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr			
420	425	430	
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys			
435	440	445	
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val			
450	455	460	
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu			
465	470	475	480
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys			
485	490	495	
Ser Glu Thr Arg Val Gln Asn Gly Arg Ser			
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<211> 1736

<212> DNA

<213> Brassica napus

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						Met	Thr	Ser	Ile	Asn	Val	Lys	Leu	Leu		
						1								5		
tac	cat	tac	gtc	ata	acc	aac	ctt	ttc	aac	ctt	tgt	ttc	ttt	cca	tta	159
Tyr	His	Tyr	Val	Ile	Thr	Asn	Leu	Phe	Asn	Leu	Cys	Phe	Phe	Pro	Leu	
10															25	
15																
acg	gcg	atc	gtc	gcc	gga	aaa	gcc	tat	ctt	acc	ata	gac	gat	ctt	cac	207
Thr	Ala	Ile	Val	Ala	Gly	Lys	Ala	Tyr	Leu	Thr	Ile	Asp	Asp	Leu	His	
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cac	tta	tac	tat	tcc	tat	ctc	caa	cac	acc	ctc	ata	acc	att	gct	cca	255
His	Leu	Tyr	Tyr	Ser	Tyr	Leu	Gln	His	Asn	Leu	Ile	Thr	Ile	Ala	Pro	
45															55	
ctc	ttg	gcc	ttc	acc	gtt	ttc	ggt	tcg	gtt	ctc	tac	atc	gca	acc	cg	303
Leu	Leu	Ala	Phe	Thr	Val	Phe	Gly	Ser	Val	Leu	Tyr	Ile	Ala	Thr	Arg	
60															70	
ccc	aaa	ccg	gtt	tac	ctc	gtg	gag	tac	tca	tgc	tac	ctt	cca	cca	acg	351
Pro	Lys	Pro	Val	Tyr	Leu	Val	Glu	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Thr	
75															85	
cat	tgt	aga	tca	agt	atc	tcc	aag	gtc	atg	gat	atc	ttt	ttc	caa	gta	399
His	Cys	Arg	Ser	Ser	Ile	Ser	Lys	Val	Met	Asp	Ile	Phe	Phe	Gln	Val	
90															105	
aga	aaa	gct	gat	cct	tct	cg	aac	ggc	acg	tgc	gat	gac	tcg	ttc	tgg	447
Arg	Lys	Ala	Asp	Pro	Ser	Arg	Asn	Gly	Thr	Cys	Asp	Asp	Ser	Ser	Trp	
110															120	
ctt	gac	ttc	ttg	agg	aag	att	caa	gaa	cgt	tca	ggt	cta	ggc	gat	gaa	495
Leu	Asp	Phe	Leu	Arg	Lys	Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	
125															135	
acc	cac	ggg	ccc	gag	ggg	ctg	ctt	cag	gtc	cct	ccc	cg	aag	act	ttt	543
Thr	His	Gly	Pro	Glu	Gly	Leu	Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	
140															150	
gcg	cgc	gct	cgt	gaa	gag	acg	gag	caa	gtt	atc	att	ggt	gct	cta	gaa	591
Ala	Arg	Ala	Arg	Glu	Glu	Thr	Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	
155															165	
aat	cta	ttc	aag	aac	acc	aat	gtt	aac	cct	aaa	gat	ata	ggt	ata	ctt	639
Asn	Leu	Phe	Lys	Asn	Thr	Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	
170															185	
gtg	gtg	aac	tca	agc	atg	ttt	aat	cca	act	cct	tcg	ctc	tcc	gct	atg	687

Val Val Asn Ser Ser Met Phe Asn Pro Thr Pro Ser Leu Ser Ala Met			
190	195	200	
gtc gtt aac act ttc aag ctc cga agc aac gta aga agc ttt aac ctt			735
Val Val Asn Thr Phe Lys Leu Arg Ser Asn Val Arg Ser Phe Asn Leu			
205	210	215	
ggt ggc atg ggt tgt agt gcc ggc gtt ata gcc att gat cta gca aag			783
Gly Gly Met Gly Cys Ser Ala Gly Val Ile Ala Ile Asp Leu Ala Lys			
220	225	230	
gac ttg ttg cat gtc cat aaa aat acg tat gct ctt gtg gtg agc aca			831
Asp Leu Leu His Val His Lys Asn Thr Tyr Ala Leu Val Val Ser Thr			
235	240	245	
gag aac atc act tat aac att tac gct ggt gat aat agg tcc atg atg			879
Glu Asn Ile Thr Tyr Asn Ile Tyr Ala Gly Asp Asn Arg Ser Met Met			
250	255	260	265
gtt tca aat tgc ttg ttc cgt gtt ggt ggg gcc gct att ttg ctc tcc			927
Val Ser Asn Cys Leu Phe Arg Val Gly Gly Ala Ala Ile Leu Leu Ser			
270	275	280	
aac aag cct aga gat cgt aga cgg tcc aag tac gag cta gtt cac acg			975
Asn Lys Pro Arg Asp Arg Arg Ser Lys' Tyr Glu Leu Val His Thr			
285	290	295	
gtt cga acg cat acc gga gct gac gac aag tct ttt cgt tgc gtg caa			1023
Val Arg Thr His Thr Gly Ala Asp Asp Lys Ser Phe Arg Cys Val Gln			
300	305	310	
caa gga gac gat gag aac ggc caa acc gga gtg agt ttg tcc aag gac			1071
Gln Gly Asp Asp Glu Asn Gly Gln Thr Gly Val Ser Leu Ser Lys Asp			
315	320	325	
ata acc gat gtt gct ggt cga acg gtt aag aaa aac ata gca acg ctg			1119
Ile Thr Asp Val Ala Gly Arg Thr Val Lys Lys Asn Ile Ala Thr Leu			
330	335	340	345
ggt ccg ttg att ctt ccg tta agc gag aaa ctt ctt ttt ttc gtt acc			1167
Gly Pro Leu Ile Leu Pro Leu Ser Glu Lys Leu Leu Phe Phe Val Thr			
350	355	360	
ttc atg ggc aag aaa ctt ttc aaa gac gaa atc aaa cat tat tac gtc			1215
Phe Met Gly Lys Lys Leu Phe Lys Asp Glu Ile Lys His Tyr Tyr Val			
365	370	375	
ccg gac ttc aag ctt gct atc gac cat ttt tgt ata cat gcc gga ggc			1263
Pro Asp Phe Lys Leu Ala Ile Asp His Phe Cys Ile His Ala Gly Gly			
380	385	390	
aaa gcc gtg att gat gtg cta gag aag aac cta ggc cta gca ccg atc			1311
Lys Ala Val Ile Asp Val Leu Glu Lys Asn Leu Gly Leu Ala Pro Ile			
395	400	405	
gat gta gag gca tca aga tca acg tta cat aga ttt gga aac act tca			1359

Asp Val Glu Ala Ser Arg Ser Thr Leu His Arg Phe Gly Asn Thr Ser				
410	415	420	425	
tct agc tca ata tgg tat gag ttg gca tac ata gaa ccc aaa gga agg				1407
Ser Ser Ser Ile Trp Tyr Glu Leu Ala Tyr Ile Glu Pro Lys Gly Arg				
430	435	440		
atg aag aaa ggt aat aaa gtt tgg cag att gct tta ggg tca ggc ttt				1455
Met Lys Lys Gly Asn Lys Val Trp Gln Ile Ala Leu Gly Ser Gly Phe				
445	450	455		
aag tgt aac agt gca gtt tgg gtg gct cta aac aat gtc aaa gct tca				1503
Lys Cys Asn Ser Ala Val Trp Val Ala Leu Asn Asn Val Lys Ala Ser				
460	465	470		
aca aat agt cct tgg gaa cac tgc atc gac aga tac ccg gtt aaa att				1551
Thr Asn Ser Pro Trp Glu His Cys Ile Asp Arg Tyr Pro Val Lys Ile				
475	480	485		
gat tct gat tca ggt aag tca gag act cgt gtc cca aac ggt cgg tcc				1599
Asp Ser Asp Ser Gly Lys Ser Glu Thr Arg Val Pro Asn Gly Arg Ser				
490	495	500	505	
taataaatga tgtttgctct ctttcgtttc tttttattgg ttataataat ttgatggcca				1659
cgatgtttct cttgtttgtt atgaataaaag aatcccacgg tgttctagta aaaaaaaaaa				1719
aaaaaaaaaa aaaaaaaaaa				1736
<210> 6				
<211> 505				
<212> PRT				
<213> Brassica napus				
<400> 6				
Met Thr Ser Ile Asn Val Lys Leu Leu Tyr His Tyr Val Ile Thr Asn				
1	5	10	15	
Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys				
20	25	30		
Ala Tyr Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr Leu				
35	40	45		
Gln His Asn Leu Ile Thr Ile Ala Pro Leu Leu Ala Phe Thr Val Phe				
50	55	60		
Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu Val				
65	70	75	80	
Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile Ser				
85	90	95		
Lys Val Met Asp Ile Phe Phe Gln Val Arg Lys Ala Asp Pro Ser Arg				
100	105	110		
Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys Ile				
115	120	125		
Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly Leu				
130	135	140		
Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Arg Ala Arg Glu Glu Thr				
145	150	155	160	
Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr Asn				
165	170	175		
Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met Phe				

180	185	190
Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys Leu		
195	200	205
Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser Ala		
210	215	220
Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His Lys		
225	230	235
Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn Ile		
245	250	255
Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe Arg		
260	265	270
Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Arg Asp Arg Arg		
275	280	285
Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly Ala		
290	295	300
Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn Gly		
305	310	315
Gln Thr Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly Arg		
325	330	335
Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro Leu		
340	345	350
Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu Phe		
355	360	365
Lys Asp Glu Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala Ile		
370	375	380
Asp His Phe Cys Ile His Ala Gly Gly Lys Ala Val Ile Asp Val Leu		
385	390	395
Glu Lys Asn Leu Gly Leu Ala Pro Ile Asp Val Glu Ala Ser Arg Ser		
405	410	415
Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr Glu		
420	425	430
Leu Ala Tyr Ile Glu Pro Lys Gly Arg Met Lys Lys Gly Asn Lys Val		
435	440	445
Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val Trp		
450	455	460
Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu His		
465	470	475
Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys Ser		
485	490	495
Glu Thr Arg Val Pro Asn Gly Arg Ser		
500	505	

<210> 7
 <211> 1521
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 5' 342 bp from A. thaliana FAE1 (SEQ ID NO:1) and
 3' 1179 bp from B. napus elongase KCS (SEQ ID
 NO:3); designated At114

<221> CDS
 <222> (1)...(1518)

<400> 7

atg acg tcc gtt aac gtt aag ctc ctt tac cgt tat gtc tta acc aac Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn	48
1 5 10 15	
ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys	96
20 25 30	
gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu	144
35 40 45	
caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe	192
50 55 60	
ggg ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val	240
65 70 75 80	
gac tac tcg tgt tac ctt ccg cca ccg cat ctc aaa gtt agt gtc tct Asp Tyr Ser Cys Tyr Leu Pro Pro His Leu Lys Val Ser Val Ser	288
85 90 95	
aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser	336
100 105 110	
cgg aac ggc acg tgt gat gat tcg tcg tgg ctt gac ttc ttg agg aag Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys	384
115 120 125	
att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly	432
130 135 140	
ctg ctt cag gtc cct ccc cgg aag act ttt gcg gcg gcg cgt gaa gag Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Arg Glu Glu	480
145 150 155 160	
acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr	528
165 170 175	
aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met	576
180 185 190	
ttt aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys	624
195 200 205	
ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser	672
210 215 220	

gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat		720
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His		
225	230	235
240		
aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac		768
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn		
245	250	255
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc		816
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe		
260	265	270
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt		864
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg		
275	280	285
aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga		912
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly		
290	295	300
gct gac ggc aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac		960
Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn		
305	310	315
320		
ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt		1008
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly		
325	330	335
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg		1056
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro		
340	345	350
tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt		1104
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu		
355	360	365
ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct		1152
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala		
370	375	380
att gac cat ttt tgt ata cat gtc ggc aga gca gtc gtg att gat gtg		1200
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val		
385	390	395
400		
cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga		1248
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg		
405	410	415
tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat		1296
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr		
420	425	430
440		
gag ttg gca tac ata gaa rca aaa gga agg atg aag aaa ggt aat aaa		1344
Glu Leu Ala Tyr Ile Glu Xaa Lys Gly Arg Met Lys Lys Gly Asn Lys		
435	440	445

gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt	1392
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val	
450 455 460	
tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa	1440
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu	
465 470 475 480	
cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag	1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys	
485 490 495	
tca gag act cgt gtc cca aac ggt cgg tcc taa	1521
Ser Glu Thr Arg Val Pro Asn Gly Arg Ser	
500 505	

<210> 8
 <211> 506
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> VARIANT
 <222> (0)...(0)
 <223> Xaa = Ala or Thr

<223> 5' 114 amino acids from A. thaliana FAE1 (SEQ ID NO:2) and 3' 392 amino acids from B. napus elongase KCS (SEQ ID NO:4); designated At114

<400> 8

Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn	
1 5 10 15	
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys	
20 25 30	
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu	
35 40 45	
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe	
50 55 60	
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val	
65 70 75 80	
Asp Tyr Ser Cys Tyr Leu Pro Pro His Leu Lys Val Ser Val Ser	
85 90 95	
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser	
100 105 110	
Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys	
115 120 125	
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly	
130 135 140	
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu	
145 150 155 160	
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr	
165 170 175	
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met	
180 185 190	

Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
 195 200 205
 Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
 210 215 220
 Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
 225 230 235 240
 Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn
 245 250 255
 Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
 260 265 270
 Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg
 275 280 285
 Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly
 290 295 300
 Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn
 305 310 315 320
 Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly
 325 330 335
 Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
 340 345 350
 Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
 355 360 365
 Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
 370 375 380
 Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
 385 390 395 400
 Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
 420 425 430
 Glu Leu Ala Tyr Ile Glu Xaa Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
 465 470 475 480
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
 485 490 495
 Ser Glu Thr Arg Val Pro Asn Gly Arg Ser
 500 505

<210> 9
 <211> 1518
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 5' 222 bp from A. thaliana FAE1 (SEQ ID NO:1) and
 3' 1296 bp from B. napus elongase KCS (SEQ ID
 NO:3); designated At74

<221> CDS
 <222> (1) ... (1515)

<400> 9
 atg acg tcc gtt aac gtt aag ctc ctt tac cgt tac gtc tta acc aac

Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn			
1	5	10	15
ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa			96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys			
20	25	30	
gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc			144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu			
35	40	45	
caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc			192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe			
50	55	60	
ggg ttg gtt ctc tac atc gta acc cga ccc aaa ccg gtt tac ctc gtt			240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Lys Pro Val Tyr Leu Val			
65	70	75	80
gag tac tca tgc tac ctt cca cca acg cat tgt aga tca agt atc tcc			288
Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile Ser			
85	90	95	
aag gtc atg gat atc ttt tat caa gta aga aaa gct gat cct tct cgg			336
Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser Arg			
100	105	110	
aac ggc acg tgc gat gac tcg tcg tgg ctt gac ttc ttg agg aag att			384
Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys Ile			
115	120	125	
caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg ctg			432
Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly Leu			
130	135	140	
ctt cag gtc cct ccc cgg aag act ttt gcg gcg gcg cgt gaa gag acg			480
Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu Thr			
145	150	155	160
gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc aac			528
Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr Asn			
165	170	175	
gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg ttt			576
Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met Phe			
180	185	190	
aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag ctc			624
Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys Leu			
195	200	205	
cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt gcc			672
Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser Ala			
210	215	220	
ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat aaa			720

Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His Lys			
225	230	235	240
aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac att			768
Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn Ile			
245	250	255	
tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc cgt			816
Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe Arg			
260	265	270	
gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt aga			864
Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg Arg			
275	280	285	
cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga gct			912
Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly Ala			
290	295	300	
gac ggc aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac ggc			960
Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn Gly			
305	310	315	320
aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt cga			1008
Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly Arg			
325	330	335	
acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg tta			1056
Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro Leu			
340	345	350	
agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt ttc			1104
Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu Phe			
355	360	365	
aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct att			1152
Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala Ile			
370	375	380	
gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg cta			1200
Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val Leu			
385	390	395	400
gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga tca			1248
Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg Ser			
405	410	415	
acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat gag			1296
Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr Glu			
420	425	430	
ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa gtt			1344
Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys Val			
435	440	445	
tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt tgg			1392

Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val Trp
 450 455 460

gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa cac 1440
 Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu His
 465 470 475 480

tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag tca 1488
 Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys Ser
 485 490 495

gag act cgt gtc caa aac ggt cgg tcc taa 1518
 Glu Thr Arg Val Gln Asn Gly Arg Ser
 500 505

<210> 10
 <211> 505
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 5' 74 amino acids from A. thaliana FAE1 (SEQ ID
 NO:2) and 3' 431 amino acids from B. napus
 elongase KCS (SEQ ID NO:4); designated At74

<400> 10
 Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
 1 5 10 15
 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
 20 25 30
 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
 35 40 45
 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
 50 55 60
 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Lys Pro Val Tyr Leu Val
 65 70 75 80
 Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile Ser
 85 90 95
 Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser Arg
 100 105 110
 Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys Ile
 115 120 125
 Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly Leu
 130 135 140
 Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu Thr
 145 150 155 160
 Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr Asn
 165 170 175
 Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met Phe
 180 185 190
 Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys Leu
 195 200 205
 Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser Ala
 210 215 220
 Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His Lys

225	230	235	240												
Asn	Thr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn	Ile	
245							250				255				
Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe	Arg
260							265				270				
Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg	Arg
275							280				285				
Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly	Ala
290							295				300				
Asp	Gly	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn	Gly
305							310				315			320	
Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	Gly	Arg
							325			330			335		
Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro	Leu
							340			345			350		
Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr	Phe	Met	Gly	Lys	Lys	Leu	Phe
							355			360			365		
Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	Leu	Ala	Ile
							370			375			380		
Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	Asp	Val	Leu
							385			390			395		400
Glu	Lys	Asn	Leu	Ala	Leu	Ala	Pro	Ile	Asp	Val	Glu	Ala	Ser	Arg	Ser
							405			410			415		
Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ile	Trp	Tyr	Glu	
							420			425			430		
Leu	Ala	Tyr	Ile	Glu	Ala	Lys	Gly	Arg	Met	Lys	Lys	Gly	Asn	Lys	Val
							435			440			445		
Trp	Gln	Ile	Ala	Leu	Gly	Ser	Gly	Phe	Lys	Cys	Asn	Ser	Ala	Val	Trp
							450			455			460		
Val	Ala	Leu	Asn	Asn	Val	Lys	Ala	Ser	Thr	Asn	Ser	Pro	Trp	Glu	His
							465			470			475		480
Cys	Ile	Asp	Arg	Tyr	Pro	Val	Lys	Ile	Asp	Ser	Asp	Ser	Gly	Lys	Ser
							485			490			495		
Glu	Thr	Arg	Val	Gln	Asn	Gly	Arg	Ser							
							500			505					

<210> 11
<211> 1521
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' 342 bp from A. thaliana FAE1 (SEQ ID NO:1) and
3' 1179 bp from B. napus elongase KCS (SEQ ID
NO:3) having mutations at positions 271, 272 and
275; designated At114 L91C K92R

<221> CDS
<222> (1)...(1518)

<400> 11
atg acg tcc gtt aac gtt aag ctc ctt tac cgt tat gtc tta acc aac
Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
1 5 10 15

ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa

48

96

Phe	Phe	Asn	Leu	Cys	Leu	Phe	Pro	Leu	Thr	Ala	Phe	Leu	Ala	Gly	Lys	
																20
																25
																30
gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc															144	
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu	
																35
																40
																45
caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc															192	
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe	
																50
																55
																60
ggg ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt															240	
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Asn	Pro	Val	Tyr	Leu	Val	
																65
																70
																75
																80
gac tac tcg tgt tac ctt ccg cca ccg cat tgc aga gtt agt gtc tct															288	
Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Pro	His	Cys	Arg	Val	Ser	Val	Ser	
																85
																90
																95
aaa gtc atg gat att ttc taccaa ata aga aaa gct gat act tct tca															336	
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Ile	Arg	Lys	Ala	Asp	Thr	Ser	Ser	
																100
																105
																110
cgaaacggc acg tgt gat aat tcg tcg tgg ctt gac ttc ttg agg aag															384	
Arg	Asn	Gly	Thr	Cys	Asp	Asn	Ser	Ser	Trp	Leu	Asp	Phe	Leu	Arg	Lys	
																115
																120
																125
att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg															432	
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	Glu	Gly	
																130
																135
																140
ctg ctt cag gtc cct ccc cgg aag act ttt gcg gcg gcg cgt gaa gag															480	
Leu	Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Arg	Glu	Glu		
																145
																150
																155
																160
acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc															528	
Thr	Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr	
																165
																170
																175
aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg															576	
Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met	
																180
																185
																190
ttt aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag															624	
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys	
																195
																200
																205
ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt															672	
Leu	Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	
																210
																215
																220
gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat															720	
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His	
																225
																230
																235
																240
aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac															768	

Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn			
245	250	255	
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc			816
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe			
260	265	270	
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt			864
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg			
275	280	285	
aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga			912
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly			
290	295	300	
gct gac ggc aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac			960
Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn			
305	310	315	320
ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt			1008
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly			
325	330	335	
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg			1056
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro			
340	345	350	
tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt			1104
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu			
355	360	365	
ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct			1152
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala			
370	375	380	
att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg			1200
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val			
385	390	395	400
cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga			1248
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg			
405	410	415	
tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat			1296
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr			
420	425	430	
gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa			1344
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys			
435	440	445	
gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt			1392
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val			
450	455	460	
tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa			1440

Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
 465 470 475 480

cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag 1488
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
 485 490 495

tca gag act cgt gtc cca aac ggt cggt tcc taa 1521
 Ser Glu Thr Arg Val Pro Asn Gly Arg Ser
 500 505

<210> 12
 <211> 506
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 5' 114 amino acids from A. thaliana FAE1 (SEQ ID
 NO:2) and 3' 392 amino acids from B. napus
 elongase KCS (SEQ ID NO:4) having mutations at
 residues 91 and 92; designated At114 L91C K92R

<400> 12
 Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
 1 5 10 15
 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
 20 25 30
 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
 35 40 45
 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
 50 55 60
 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
 65 70 75 80
 Asp Tyr Ser Cys Tyr Leu Pro Pro His Cys Arg Val Ser Val Ser
 85 90 95
 Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser
 100 105 110
 Arg Asn Gly Thr Cys Asp Asn Ser Ser Trp Leu Asp Phe Leu Arg Lys
 115 120 125
 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly
 130 135 140
 Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu
 145 150 155 160
 Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr
 165 170 175
 Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met
 180 185 190
 Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
 195 200 205
 Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
 210 215 220
 Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
 225 230 235 240
 Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn
 245 250 255

Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
 260 265 270
 Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg
 275 280 285
 Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly
 290 295 300
 Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn
 305 310 315 320
 Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly
 325 330 335
 Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
 340 345 350
 Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
 355 360 365
 Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
 370 375 380
 Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
 385 390 395 400
 Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
 420 425 430
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
 465 470 475 480
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
 485 490 495
 Ser Glu Thr Arg Val Pro Asn Gly Arg Ser
 500 505

<210> 13
<211> 1521
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' 342 bp from A. thaliana FAE1 (SEQ ID NO:1) and
 3' 1179 bp from B. napus elongase KCS (SEQ ID
 NO:3), having a mutation at position 275;
 designated At114_K92R

<221> CDS
<222> (1)...(1518)

<400> 13
 atg acg tcc gtt aac gtt aag ctc ctt tac cgt tat gtc tta acc aac
 Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
 1 5 10 15

ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa
 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
 20 25 30

48

96

gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu 35 40 45	144
caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe 50 55 60	192
ggg ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val 65 70 75 80	240
gac tac tcg tgt tac ctt ccg cca ccg cat ctc aga gtt agt gtc tct Asp Tyr Ser Cys Tyr Leu Pro Pro His Leu Arg Val Ser Val Ser 85 90 95	288
aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser 100 105 110	336
cgg aac ggc acg tgt gat gat tcg tcg tgg ctt gac ttc ttg agg aag Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys 115 120 125	384
att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly 130 135 140	432
ctg ctt cag gtc cct ccc cgg aag act ttt gcg gcg gcg cgt gaa gag Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Arg Glu Glu 145 150 155 160	480
acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr 165 170 175	528
aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met 180 185 190	576
ttt aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys 195 200 205	624
ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser 210 215 220	672
gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His 225 230 235 240	720
aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn 245 250 255	768

att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe 260 265 270	816
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg 275 280 285	864
aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly 290 295 300	912
gct gac ggc aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn 305 310 315 320	960
ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly 325 330 335	1008
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro 340 345 350	1056
tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu 355 360 365	1104
ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala 370 375 380	1152
att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val 385 390 395 400	1200
cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga Leu Glu Lys Asn Leu Ala Pro Ile Asp Val Glu Ala Ser Arg 405 410 415	1248
tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr 420 425 430	1296
gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys 435 440 445	1344
gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val 450 455 460	1392
tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu 465 470 475 480	1440

cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag	1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys	
485	490
	495

tca gag act cgt gtc cca aac ggt cggt tcc taa	1521
Ser Glu Thr Arg Val Pro Asn Gly Arg Ser	
500	505

<210> 14
<211> 506
<212> PRT
<213> Artificial Sequence

<220>
<223> 5' 114 amino acids from A. thaliana FAE1 (SEQ ID NO:2) and 3' 392 amino acids from B. napus elongase KCS (SEQ ID NO:4), having a mutation at position 92; designated At114 K92R

<400> 14			
Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn			
1	5	10	15
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys			
20	25	30	
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu			
35	40	45	
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe			
50	55	60	
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val			
65	70	75	80
Asp Tyr Ser Cys Tyr Leu Pro Pro His Leu Arg Val Ser Val Ser			
85	90	95	
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser			
100	105	110	
Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys			
115	120	125	
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly			
130	135	140	
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu			
145	150	155	160
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr			
165	170	175	
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met			
180	185	190	
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys			
195	200	205	
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser			
210	215	220	
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His			
225	230	235	240
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn			
245	250	255	
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe			
260	265	270	
Arg Val Gly Gly Ala Ala Ile Leu Ser Asn Lys Pro Gly Asp Arg			

275	280	285
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly		
290	295	300
Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn		
305	310	315
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly		
325	330	335
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro		
340	345	350
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu		
355	360	365
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala		
370	375	380
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val		
385	390	395
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg		
405	410	415
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr		
420	425	430
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys		
435	440	445
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val		
450	455	460
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu		
465	470	475
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys		
485	490	495
Ser Glu Thr Arg Val Pro Asn Gly Arg Ser		
500	505	

<210> 15

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 342 bp from A. thaliana FAE1 (SEQ ID NO:1) and
3' 1179 bp from B. napus elongase KCS (SEQ ID
NO:3), having a mutation at position 920;
designated At114 G307D; hypothetical

<221> CDS

<222> (1)...(1518)

<400> 15

atg acg tcc gtt aac gtt aag ctc ctt tac cgt tat gtc tta acc aac				48
Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn				
1	5	10	15	

ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa				96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys				
20	25	30		

gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc				144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu				
35	40	45		

caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc		192	
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe			
50	55	60	
ggt ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt		240	
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val			
65	70	75	80
gac tac tcg tgt tac ctt ccg cca ccg cat ctc aaa gtt agt gtc tct		288	
Asp Tyr Ser Cys Tyr Leu Pro Pro His Leu Lys Val Ser Val Ser			
85	90	95	
aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca		336	
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser			
100	105	110	
cgg aac ggc acg tgt gat tcg tcg tgg ctt gac ttc ttg agg aag		384	
Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys			
115	120	125	
att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg		432	
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly			
130	135	140	
ctg ctt cag gtc cct ccc cg ^g aag act ttt g ^c g ^c g ^c cgt gaa gag		480	
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu			
145	150	155	160
acg gag caa gtt atc att ggt g ^c g ^c aat cta ttc aag aac acc		528	
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr			
165	170	175	
aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg		576	
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met			
180	185	190	
ttt aat cca act cca tcg ctc tcc g ^c g ^c atg g ^c gtt aac act ttc aag		624	
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys			
195	200	205	
ctc cga agc aac gta aga agc ttt aac ctt ggt g ^c atg g ^c ggt tgt agt		672	
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser			
210	215	220	
gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat		720	
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His			
225	230	235	240
aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac		768	
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn			
245	250	255	
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc		816	
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe			
260	265	270	

cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt		864
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg		
275	280	285
aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga		912
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly		
290	295	300
gct gac gac aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac		960
Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn		
305	310	315
320		
ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt		1008
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly		
325	330	335
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg		1056
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro		
340	345	350
tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt		1104
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu		
355	360	365
ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct		1152
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala		
370	375	380
att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg		1200
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val		
385	390	395
400		
cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga		1248
Leu Glu Lys Asn Leu Ala Pro Ile Asp Val Glu Ala Ser Arg		
405	410	415
tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat		1296
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr		
420	425	430
gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa		1344
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys		
435	440	445
gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt		1392
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val		
450	455	460
tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa		1440
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu		
465	470	475
480		
cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag		1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys		
485	490	495

tca gag act cgt gtc caa aac ggt cggt tcc taa 1521
 Ser Glu Thr Arg Val Gln Asn Gly Arg Ser
 500 505

<210> 16
 <211> 506
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 5' 114 amino acids from A. thaliana FAE1 (SEQ ID NO:2) and 3' 392 amino acids from B. napus elongase KCS (SEQ ID NO:4) having mutation at residue 307; designated At114 G307D; hypothetical

<400> 16
 Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
 1 5 10 15
 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
 20 25 30
 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
 35 40 45
 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
 50 55 60
 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
 65 70 75 80
 Asp Tyr Ser Cys Tyr Leu Pro Pro His Leu Lys Val Ser Val Ser
 85 90 95
 Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser
 100 105 110
 Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys
 115 120 125
 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly
 130 135 140
 Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu
 145 150 155 160
 Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr
 165 170 175
 Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met
 180 185 190
 Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
 195 200 205
 Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
 210 215 220
 Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
 225 230 235 240
 Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn
 245 250 255
 Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
 260 265 270
 Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg
 275 280 285
 Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly
 290 295 300

Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn
 305 310 315 320
 Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly
 325 330 335
 Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
 340 345 350
 Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
 355 360 365
 Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
 370 375 380
 Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
 385 390 395 400
 Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr
 420 425 430
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
 465 470 475 480
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
 485 490 495
 Ser Glu Thr Arg Val Gln Asn Gly Arg Ser
 500 505

<210> 17
 <211> 1518
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 5' 222 bp from A. thaliana FAE1 (SEQ ID NO:1) and
 3' 1296 bp from B. napus elongase KCS (SEQ ID
 NO:3) having a mutation at position 917;
 designated At74 G306D; hypothetical

<221> CDS
 <222> (1)...(1515)

<400> 17

atg acg tcc gtt aac gtt aag ctc ctt tac cgt tac gtc tta acc aac	48
Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn	
1 5 10 15	
ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa	96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys	
20 25 30	
gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc	144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu	
35 40 45	
caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc	192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe	

50	55	60	
ggt ttg gtt ctc tac atc gta acc cga ccc aaa ccg gtt tac ctc gtt Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Lys Pro Val Tyr Leu Val	65	70	75 80 240
gag tac tca tgc tac ctt cca cca acg cat tgt aga tca agt atc tcc Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile Ser	85	90	95 288
aag gtc atg gat atc ttt tat caa gta aga aaa gct gat cct tct cgg Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser Arg	100	105	110 336
aac ggc acg tgc gat gac tcg tcg tgg ctt gac ttc ttg agg aag att Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys Ile	115	120	125 384
caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg ctg Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly Leu	130	135	140 432
ctt cag gtc cct ccc cgg aag act ttt gcg gcg gcg cgt gaa gag acg Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Arg Glu Glu Thr	145	150	155 160 480
gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc aac Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr Asn	165	170	175 528
gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg ttt Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met Phe	180	185	190 576
aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag ctc Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys Leu	195	200	205 624
cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt gcc Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser Ala	210	215	220 672
ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat aaa Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His Lys	225	230	235 240 720
aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac att Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn Ile	245	250	255 768
tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc cgt Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe Arg	260	265	270 816
gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt aga Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg Arg			864

275	280	285	
cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga gct Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly Ala 290 295 300			912
gac gac aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac ggc Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn Gly 305 310 315 320			960
aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt cga Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly Arg 325 330 335			1008
acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg tta Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro Leu 340 345 350			1056
agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt ttc Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu Phe 355 360 365			1104
aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct att Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala Ile 370 375 380			1152
gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg cta Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val Leu 385 390 395 400			1200
gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga tca Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg Ser 405 410 415			1248
acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat gag Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr Glu 420 425 430			1296
ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa gtt Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys Val 435 440 445			1344
tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt tgg Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val Trp 450 455 460			1392
gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa cac Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu His 465 470 475 480			1440
tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag tca Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys Ser 485 490 495			1488
gag act cgt gtc caa aac ggt cgg tcc taa Glu Thr Arg Val Gln Asn Gly Arg Ser			1518

500

505

<210> 18
 <211> 505
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 5' 74 amino acids from A. thaliana FAE1 (SEQ ID NO:2) and 3' 431 amino acids from B. napus elongase KCS (SEQ ID NO:4) having a mutation at residue 306; designated At74 G306D; hypothetical

<400> 18
 Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
 1 5 10 15
 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
 20 25 30
 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
 35 40 45
 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
 50 55 60
 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Lys Pro Val Tyr Leu Val
 65 70 75 80
 Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile Ser
 85 90 95
 Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser Arg
 100 105 110
 Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys Ile
 115 120 125
 Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly Leu
 130 135 140
 Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu Thr
 145 150 155 160
 Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr Asn
 165 170 175
 Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met Phe
 180 185 190
 Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys Leu
 195 200 205
 Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser Ala
 210 215 220
 Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His Lys
 225 230 235 240
 Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn Ile
 245 250 255
 Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe Arg
 260 265 270
 Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg Arg
 275 280 285
 Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly Ala
 290 295 300
 Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn Gly
 305 310 315 320
 Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly Arg

325	330	335
Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro Leu		
340	345	350
Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu Phe		
355	360	365
Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala Ile		
370	375	380
Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val Leu		
385	390	395
Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg Ser		
405	410	415
Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr Glu		
420	425	430
Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys Val		
435	440	445
Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val Trp		
450	455	460
Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu His		
465	470	475
Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys Ser		
485	490	495
Glu Thr Arg Val Gln Asn Gly Arg Ser		
500	505	

<210> 19

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 342 bp from A. thaliana FAE1 (SEQ ID NO:1) and
 3' 1179 bp from B. napus elongase KCS (SEQ ID
 NO:3) having mutations at positions 271, 272, 275
 and 920; designated At114 L91C K92R G307D;
 hypothetical

<221> CDS

<222> (1)...(1518)

<400> 19

atg acg tcc gtt aac gtt aag ctc ctt tac cgt tat gtc tta acc aac			48
Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn			
1	5	10	15

ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa			96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys			
20	25	30	

gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc			144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu			
35	40	45	

caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc			192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe			
50	55	60	

ggt ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt			240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val			
65	70	75	80
gac tac tcg tgt tac ctt ccg cca ccg cat tgc aga gtt agt gtc tct			288
Asp Tyr Ser Cys Tyr Leu Pro Pro His Cys Arg Val Ser Val Ser			
85	90	95	
aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca			336
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser			
100	105	110	
cgg aac ggc acg tgt gat aat tcg tcg tgg ctt gac ttc ttg agg aag			384
Arg Asn Gly Thr Cys Asp Asn Ser Ser Trp Leu Asp Phe Leu Arg Lys			
115	120	125	
att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg			432
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly			
130	135	140	
ctg ctt cag gtc cct ccc cg aag act ttt gcg gcg gct gaa gag			480
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu			
145	150	155	160
acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc			528
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr			
165	170	175	
aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg			576
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met			
180	185	190	
ttt aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag			624
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys			
195	200	205	
ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt			672
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser			
210	215	220	
gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat			720
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His			
225	230	235	240
aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac			768
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn			
245	250	255	
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc			816
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe			
260	265	270	
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt			864
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg			
275	280	285	

aga ccg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga 912
 Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly
 290 295 300

 gct gac gac aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac 960
 Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn
 305 310 315 320

 ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt 1008
 Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly
 325 330 335

 cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg 1056
 Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
 340 345 350

 tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt 1104
 Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
 355 360 365

 ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct 1152
 Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
 370 375 380

 att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg 1200
 Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
 385 390 395 400

 cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga 1248
 Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415

 tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat 1296
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
 420 425 430

 gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa 1344
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445

 gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt 1392
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460

 tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa 1440
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
 465 470 475 480

 cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag 1488
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
 485 490 495

 tca gag act cgt gtc caa aac ggt cgg tcc taa 1521
 Ser Glu Thr Arg Val Gln Asn Gly Arg Ser
 500 505

<210> 20
 <211> 506
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 5' 114 amino acids from A. thaliana FAE1 (SEQ ID NO:2) and 3' 392 amino acids from B. napus elongase KCS (SEQ ID NO:4) having mutations at positions 91, 92 and 307; designated At114 L91C K92R G307D; hypothetical

<400> 20
 Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
 1 5 10 15
 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
 20 25 30
 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
 35 40 45
 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
 50 55 60
 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
 65 70 75 80
 Asp Tyr Ser Cys Tyr Leu Pro Pro His Cys Arg Val Ser Val Ser
 85 90 95
 Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser
 100 105 110
 Arg Asn Gly Thr Cys Asp Asn Ser Ser Trp Leu Asp Phe Leu Arg Lys
 115 120 125
 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly
 130 135 140
 Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Arg Glu Glu
 145 150 155 160
 Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr
 165 170 175
 Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met
 180 185 190
 Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
 195 200 205
 Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
 210 215 220
 Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
 225 230 235 240
 Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn
 245 250 255
 Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
 260 265 270
 Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg
 275 280 285
 Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly
 290 295 300
 Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn
 305 310 315 320
 Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly
 325 330 335

Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
 340 345 350
 Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
 355 360 365
 Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
 370 375 380
 Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
 385 390 395 400
 Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr
 420 425 430
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
 465 470 475 480
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
 485 490 495
 Ser Glu Thr Arg Val Gln Asn Gly Arg Ser
 500 505

<210> 21

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 342 bp from A. thaliana FAE1 (SEQ ID NO:1) and
 3' 1179 bp from B. napus elongase KCS (SEQ ID
 NO:3) having mutations at positions 275 and 920;
 designated At114 K92R G307D; hypothetical

<221> CDS

<222> (1)...(1518)

<400> 21

atg acg tcc gtt aac gtt aag ctc ctt tac cgt tat gtc tta acc aac
 Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
 1 5 10 15

48

ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa
 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
 20 25 30

96

gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc
 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
 35 40 45

144

caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc
 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
 50 55 60

192

ggt ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt
 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val

240

65	70	75	80	
gac tac tcg tgt tac ctt ccg cca ccg cat ctc aga gtt agt gtc tct				288
Asp Tyr Ser Cys Tyr Leu Pro Pro His Leu Arg Val Ser Val Ser				
85	90	95		
aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca				336
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser				
100	105	110		
cgg aac ggc acg tgt gat tgc tcg tgg ctt gac ttc ttg agg aag				384
Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys				
115	120	125		
att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg				432
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly				
130	135	140		
ctg ctt cag gtc cct ccc cg ^g aag act ttt gc ^g gc ^g cgt gaa gag				480
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu				
145	150	155	160	
acg gag caa gtt atc att ggt gc ^g cta gaa aat cta ttc aag aac acc				528
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr				
165	170	175		
aac gtt aac cct aaa gat ata ggt ata ctt gt ^g gt ^g aac tca agc atg				576
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met				
180	185	190		
ttt aat cca act cca tcg ctc tcc gc ^g atg gtc gtt aac act ttc aag				624
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys				
195	200	205		
ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt				672
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser				
210	215	220		
gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat				720
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His				
225	230	235	240	
aaa aat acg tat gct ctt gt ^g gt ^g agc aca gag aac atc act tat aac				768
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn				
245	250	255		
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc				816
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe				
260	265	270		
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt				864
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg				
275	280	285		
aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga				912
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly				

290	295	300	
gct gac gac aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn 305	310	315	960
ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly 325	330	335	1008
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro 340	345	350	1056
tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu 355	360	365	1104
ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala 370	375	380	1152
att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val 385	390	395	1200
ctc gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga Leu Glu Lys Asn Leu Ala Pro Ile Asp Val Glu Ala Ser Arg 405	410	415	1248
tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr 420	425	430	1296
gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys 435	440	445	1344
gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val 450	455	460	1392
tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu 465	470	475	1440
cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys 485	490	495	1488
tca gag act cgt gtc caa aac ggt cggt tcc taa Ser Glu Thr Arg Val Gln Asn Gly Arg Ser 500	505		1521

<211> 506
<212> PRT
<213> Artificial Sequence

<220>

<223> 5' 114 amino acids from *A. thaliana* FAE1 (SEQ ID NO:2) and 3' 392 amino acids from *B. napus* elongase KCS (SEQ ID NO:4) having mutations at positions 92 and 307; designated At114 K92R G307D; hypothetical

<400> 22

Met	Thr	Ser	Val	Asn	Val	Lys	Leu	Leu	Tyr	Arg	Tyr	Val	Leu	Thr	Asn
1					5				10					15	
Phe	Phe	Asn	Leu	Cys	Leu	Phe	Pro	Leu	Thr	Ala	Phe	Leu	Ala	Gly	Lys
					20				25					30	
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu
					35				40					45	
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe
					50				55					60	
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Asn	Pro	Val	Tyr	Leu	Val
					65				70					75	
Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Pro	His	Leu	Arg	Val	Ser	Val	Ser
					85				90					95	
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Ile	Arg	Lys	Ala	Asp	Thr	Ser	Ser
					100				105					110	
Arg	Asn	Gly	Thr	Cys	Asp	Asp	Ser	Ser	Trp	Leu	Asp	Phe	Leu	Arg	Lys
					115				120					125	
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	Glu	Gly
					130				135					140	
Leu	Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	Glu	Glu
					145				150					155	
Thr	Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr
					165				170					175	
Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met
					180				185					190	
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys
					195				200					205	
Leu	Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser
					210				215					220	
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His
					225				230					235	
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn
					245				250					255	
Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe
					260				265					270	
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg
					275				280					285	
Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly
					290				295					300	
Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn
					305				310					315	
Gly	Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	Gly
					325				330					335	
Arg	Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro
					340				345					350	

Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
 355 360 365
 Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
 370 375 380
 Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
 385 390 395 400
 Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr
 420 425 430
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
 465 470 475 480
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
 485 490 495
 Ser Glu Thr Arg Val Gln Asn Gly Arg Ser
 500 505

<210> 23

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 762 bp from A. thaliana FAE1 (SEQ ID NO:1) and
 3' 759 bp from B. napus elongase KCS (SEQ ID
 NO:3); designated At254

<221> CDS

<222> (1) ... (1518)

<400> 23

atg acg tcc gtt aac gtt aag ctc ctt tac cgt tac gtc tta acc aac	48
Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn	
1 5 10 15	

ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa	96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys	
20 25 30	

gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc	144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu	
35 40 45	

caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc	192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe	
50 55 60	

ggt ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt	240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val	
65 70 75 80	

gac tac tcg tgt tac ctt cca cca ccg cat ctc aaa gtt agt gtc tct	288
---	-----

Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser			
85	90	95	
aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca		336	
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser			
100	105	110	
cg ^g aac gt ^g gca t ^g t gat gat cc ^g tcc tc ^g c ^t c gat ttc ct ^g agg a ^g a ^g		384	
Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys			
115	120	125	
att caa gag cgt tca ggt cta ggt gat gag acg tac agt cct gag gga		432	
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly			
130	135	140	
ctc att cac gta cca cc ^g cc ^g a ^g act ttt gca g ^c tca c ^g t gaa g ^a g ^a		480	
Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu			
145	150	155	160
aca gag a ^g gtt atc atc ggt g ^c g ^c c ^t c gaa a ^a t ^t c ^t g ^a g ^a a ^a c ^c		528	
Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Glu Asn Thr			
165	170	175	
aaa gtt aac cct aga gag att ggt ata ctt gt ^g gt ^g aac tca agc atg		576	
Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met			
180	185	190	
ttt aat cca act cct tc ^g cta tcc gct atg gtc gtt aat act ttc a ^g a ^g		624	
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys			
195	200	205	
ctc c ^g a agc aac atc aaa agc ttt aat cta gga gga atg ggt t ^g t agt		672	
Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser			
210	215	220	
gct ggt gtt att gcc att gat ttg gct aaa gac ttg ttg cat gtt cat		720	
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His			
225	230	235	240
aaa aac act tat gct ctc gt ^g gt ^g agc aca gag aac atc act tat aac		768	
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn			
245	250	255	
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc		816	
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe			
260	265	270	
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt		864	
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg			
275	280	285	
aga c ^g g tcc aag tac gag cta gtt cac acg gtt c ^g a acg cat acc gga		912	
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly			
290	295	300	
gct gac ggc aag tct ttt cgt tgc gt ^g caa caa gga gac gat gag aac		960	

Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn			
305	310	315	320
ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt			1008
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly			
325	330	335	
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg			1056
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro			
340	345	350	
tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt			1104
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu			
355	360	365	
ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct			1152
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala			
370	375	380	
att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtc			1200
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val			
385	390	395	400
cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga			1248
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg			
405	410	415	
tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat			1296
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr			
420	425	430	
gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa			1344
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys			
435	440	445	
gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt			1392
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val			
450	455	460	
tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa			1440
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu			
465	470	475	480
cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag			1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys			
485	490	495	
tca gag act cgt gtc cca aac ggt cggt tcc taa			1521
Ser Glu Thr Arg Val Pro Asn Gly Arg Ser			
500	505		

<210> 24
 <211> 506
 <212> PRT
 <213> Artificial Sequence

<220>

<223> 5' 254 amino acids from A. thaliana FAE1 (SEQ ID NO:2) and 3' 252 amino acids from B. napus elongase KCS (SEQ ID NO:4); designated At254

<400> 24

Met	Thr	Ser	Val	Asn	Val	Lys	Leu	Leu	Tyr	Arg	Tyr	Val	Leu	Thr	Asn
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Phe	Phe	Asn	Leu	Cys	Leu	Phe	Pro	Leu	Thr	Ala	Phe	Leu	Ala	Gly	Lys
					20				25					30	
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu
					35				40					45	
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe
					50				55					60	
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Asn	Pro	Val	Tyr	Leu	Val
					65				70					80	
Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Pro	His	Leu	Lys	Val	Ser	Val	Ser
					85				90					95	
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Ile	Arg	Lys	Ala	Asp	Thr	Ser	Ser
					100				105					110	
Arg	Asn	Val	Ala	Cys	Asp	Asp	Pro	Ser	Ser	Leu	Asp	Phe	Leu	Arg	Lys
					115				120					125	
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	Tyr	Ser	Pro	Glu	Gly
					130				135					140	
Leu	Ile	His	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ser	Arg	Glu	Glu
					145				150					160	
Thr	Glu	Lys	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Glu	Asn	Thr
					165				170					175	
Lys	Val	Asn	Pro	Arg	Glu	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met
					180				185					190	
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys
					195				200					205	
Leu	Arg	Ser	Asn	Ile	Lys	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser
					210				215					220	
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His
					225				230					240	
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn
					245				250					255	
Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe
					260				265					270	
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg
					275				280					285	
Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly
					290				295					300	
Ala	Asp	Gly	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn
					305				310					320	
Gly	Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	Gly
					325				330					335	
Arg	Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro
					340				345					350	
Leu	Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr	Phe	Met	Gly	Lys	Lys	Leu
					355				360					365	
Phe	Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	Leu	Ala
					370				375					380	
Ile	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	Asp	Val

385	390	395	400												
Leu	Glu	Lys	Asn	Leu	Ala	Leu	Ala	Pro	Ile	Asp	Val	Glu	Ala	Ser	Arg
				405					410					415	
Ser	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ile	Trp	Tyr	
					420			425				430			
Glu	Leu	Ala	Tyr	Ile	Glu	Ala	Lys	Gly	Arg	Met	Lys	Gly	Asn	Lys	
					435			440			445				
Val	Trp	Gln	Ile	Ala	Leu	Gly	Ser	Gly	Phe	Lys	Cys	Asn	Ser	Ala	Val
					450			455			460				
Trp	Val	Ala	Leu	Asn	Asn	Val	Lys	Ala	Ser	Thr	Asn	Ser	Pro	Trp	Glu
					465			470			475			480	
His	Cys	Ile	Asp	Arg	Tyr	Pro	Val	Lys	Ile	Asp	Ser	Asp	Ser	Gly	Lys
					485			490			495				
Ser	Glu	Thr	Arg	Val	Pro	Asn	Gly	Arg	Ser						
				500				505							

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<210> 25
<211> 1521
<212> DNA
<213> Artificial Sequence
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<220>
<223> 5' 519 bp from *A. thaliana* FAE1 (SEQ ID NO:1) and
3' 1002 bp from *B. napus* elongase KCS (SEQ ID
NO:3); designated At173

<221> CDS
<222> (1) . . . (1518)

<400> 25
atg acg tcc gtt aac gtt aag ctc ctt tac cgt tac gtc tta acc aac 48
Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
1 5 10 15

ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa 96
 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
 20 25 30

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gcc tct cggtt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc 144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
35          40          45

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caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc 192
 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
 50 55 60

```

ggt ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt 240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
   65           70           75           80

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gac tac tcg tgt tac ctt cca cca ccg cat ctc aaa gtt agt gtc tct 288
 Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser
 85 90 95

aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca 336
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser

100	105	110	
cg g aac gt g gca t g gat gat cc g tcc tc g ctc gat ttc ct g agg a g Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys			384
115	120	125	
att caa gag cgt tca ggt cta ggt gat gag acg tac agt cct gag gga Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly			432
130	135	140	
ctc att cac gta cca cc g aag act ttt gca g c tca cgt gaa gag Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu			480
145	150	155	160
aca gag aag gtt atc atc ggt g c ctc gaa aat cta ttc aag aac acc Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr			528
165	170	175	
aac gtt aac cct aaa gat ata ggt ata ctt gt g gt g aac tca agc atg Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met			576
180	185	190	
ttt aat cca act cca tc g ctc tcc g c atg gtc gtt aac act ttc aag Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys			624
195	200	205	
ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt t g t g agt Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser			672
210	215	220	
gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His			720
225	230	235	240
aaa aat acg tat gct ctt gt g gt g agc aca gag aac atc act tat aac Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn			768
245	250	255	
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe			816
260	265	270	
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg			864
275	280	285	
aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly			912
290	295	300	
gct gac ggc aag tct ttt cgt tgc gt g caa caa gga gac gat gag aac Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn			960
305	310	315	320
ggc aaa atc gga gt g agt ttg tcc aag gac ata acc gat gtt gct ggt Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly			1008

325	330	335	
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro 340	345	350	1056
tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu 355	360	365	1104
ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala 370	375	380	1152
att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val 385	390	395	1200
cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg 405	410	415	1248
tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr 420	425	430	1296
gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys 435	440	445	1344
gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val 450	455	460	1392
tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu 465	470	475	1440
cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys 485	490	495	1488
tca gag act cgt gtc cma aac ggt cggt tcc taa Ser Glu Thr Arg Val Xaa Asn Gly Arg Ser 500	505		1521

<210> 26
 <211> 506
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 5' 173 amino acids from A. thaliana FAE1 (SEQ ID
 NO:2) and 3' 333 amino acids from B. napus
 elongase KCS (SEQ ID NO:4); designated At173

<221> VARIANT
 <222> (0)...(0)
 <223> Xaa = Pro or Gln

<400> 26
 Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
 1 5 10 15
 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
 20 25 30
 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
 35 40 45
 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
 50 55 60
 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
 65 70 75 80
 Asp Tyr Ser Cys Tyr Leu Pro Pro His Leu Lys Val Ser Val Ser
 85 90 95
 Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser
 100 105 110
 Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys
 115 120 125
 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly
 130 135 140
 Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu
 145 150 155 160
 Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr
 165 170 175
 Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met
 180 185 190
 Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
 195 200 205
 Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
 210 215 220
 Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
 225 230 235 240
 Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn
 245 250 255
 Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
 260 265 270
 Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg
 275 280 285
 Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly
 290 295 300
 Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn
 305 310 315 320
 Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly
 325 330 335
 Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
 340 345 350
 Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
 355 360 365
 Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
 370 375 380
 Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
 385 390 395 400

Leu	Glu	Lys	Asn	Leu	Ala	Leu	Ala	Pro	Ile	Asp	Val	Glu	Ala	Ser	Arg
				405					410					415	
Ser	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	Ile	Trp	Tyr
				420				425					430		
Glu	Leu	Ala	Tyr	Ile	Glu	Ala	Lys	Gly	Arg	Met	Lys	Lys	Gly	Asn	Lys
				435				440				445			
Val	Trp	Gln	Ile	Ala	Leu	Gly	Ser	Gly	Phe	Lys	Cys	Asn	Ser	Ala	Val
				450				455			460				
Trp	Val	Ala	Leu	Asn	Asn	Val	Lys	Ala	Ser	Thr	Asn	Ser	Pro	Trp	Glu
				465				470			475			480	
His	Cys	Ile	Asp	Arg	Tyr	Pro	Val	Lys	Ile	Asp	Ser	Asp	Ser	Gly	Lys
				485				490					495		
Ser	Glu	Thr	Arg	Val	Xaa	Asn	Gly	Arg	Ser						
				500				505							

<210> 27

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 528 bp from *B. napus* elongase KCS (SEQ ID NO:3)
and 3' 993 bp from *A. thaliana* FAE1 (SEQ ID NO:1);
designated Bn176

<221> CDS

<222> (1)...(1518)

<400> 27

atg acg tcc att aac gta aag ctc ctt tac cat tac gtc ata acc aac
Met Thr Ser Ile Asn Val Lys Leu Leu Tyr His Tyr Val Ile Thr Asn
1 5 10 15

48

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  ctt ttc aac ctt tgc ttc ttt ccg tta acg gcg atc gtc gcc gga aaa
  Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys
              20          25          30

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96

gcc tat cg³⁵ ctt acc ata gac gat ctt cac cac tta tac tat tcc tat
Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr
35 40 45

144

ctc caa cac aac ctc ata acc atc gct cca ctc ttt gcc ttc acc gtt
 Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val
 50 55 60

192

```

ttc ggt tcg gtt ctc tac atc gca acc cgg ccc aaa ccg gtt tac ctc
Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu
   65           70           75           80

```

240

gtt gag tac tca tgc tac ctt cca cca acg cat tgt aga tca agt atc
 Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile
 85 90 95

288

tcc aag gtc atg gat atc ttt tat caa gta aga aaa gct gat cct tct
Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser
100 105 110

cg ^g a ^a c ^c g ^g c ^a t ^g c ^g t ^c g ^t c ^g t ^g c ^t g ^a t ^c t ^t c ^g t ^t g ^a g ^g a ^a g ^g	384
Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys	
115 120 125	
att c ^a a ^a c ^g t ^c a ^g g ^g t ^c a ^g g ^g c ^a t ^a c ^c g ^g c ^c g ^g c ^g t ^a g ^g g ^g	432
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly	
130 135 140	
ct ^g c ^t t ^t c ^a g ^c t ^c c ^c c ^g a ^a g ^c a ^t t ^t t ^t g ^c g ^c g ^c c ^g t ^a g ^a g ^g	480
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu	
145 150 155 160	
ac ^g g ^a c ^a a ^a g ^t t ^c a ^t t ^g g ^c t ^a g ^a a ^a t ^t c ^a t ^t a ^a g ^a a ^a c ^c	528
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr	
165 170 175	
aaa g ^t t ^t a ^a c ^c t ^t a ^g a ^a g ^g t ^t g ^a t ^a c ^t t ^t g ^t g ^t a ^a c ^g a ^c t ^g	576
Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met	
180 185 190	
t ^t t ^t a ^a c ^c a ^a c ^t t ^c g ^t c ^a t ^c t ^c g ^c t ^t a ^t a ^a c ^t t ^t a ^a g ^a	624
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys	
195 200 205	
ct ^c c ^g a ^a a ^a c ^t t ^c a ^a a ^a g ^c t ^t a ^a t ^t c ^t g ^t g ^t a ^t g ^t t ^t a ^t g ^t	672
Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser	
210 215 220	
g ^c t ^t g ^t g ^t a ^t t ^t g ^c c ^c a ^t g ^t t ^t g ^c t ^t a ^a g ^c t ^t t ^t c ^a t ^t g ^t t ^t	720
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His	
225 230 235 240	
aaa a ^a a ^a c ^c a ^t t ^t g ^c t ^t g ^t g ^c a ^c t ^t g ^a a ^a c ^t a ^c a ^a c ^c g ^g	768
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Gly	
245 250 255	
att t ^t a ^t g ^c t ^t g ^a a ^a t ^a g ^c a ^t g ^t g ^t a ^t g ^c a ^t t ^t g ^t t ^t	816
Ile Tyr Ala Gly Glu Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe	
260 265 270	
c ^g t ^t g ^t g ^t g ^g g ^c c ^c a ^t t ^t t ^t c ^t t ^c a ^a a ^a g ^c t ^c g ^g a ^c c ^g	864
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Ser Gly Asp Arg	
275 280 285	
aga c ^g t ^c c ^c a ^a g ^t t ^t c ^a a ^c c ^g g ^t c ^g a ^c a ^c t ^t a ^t g ^g	912
Arg Arg Ser Lys Tyr Lys Leu Val His Thr Val Arg Thr His Thr Gly	
290 295 300	
g ^c t ^t g ^t a ^a g ^t t ^t t ^t c ^a t ^t g ^t c ^a c ^a g ^a t ^t g ^t a ^t g ^t g ^a	960
Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Glu Asp Asp Glu Ser	
305 310 315 320	
g ^g c ^{aa} a ^t c ^c g ^a g ^t t ^t c ^t g ^c t ^a a ^a c ^c a ^a t ^t g ^c g ^g	1008
Gly Lys Ile Gly Val Cys Leu Ser Lys Asp Ile Thr Asn Val Ala Gly	
325 330 335	

aca aca ctt acg aaa aat ata gca aca ttg ggt ccg ttg att ctt cct	1056
Thr Thr Leu Thr Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro	
340 345 350	
tta agc gaa aag ttt ctt ttt ttc gct acc ttc gtc gcc aag aaa ctt	1104
Leu Ser Glu Lys Phe Leu Phe Ala Thr Phe Val Ala Lys Lys Leu	
355 360 365	
cta aag gat aaa atc aag cat tac tat gtt ccg gat ttc aag ctt gct	1152
Leu Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala	
370 375 380	
gtt gac cat ttc tgt att cat gcc gga ggc aga gcc gtg atc gat gag	1200
Val Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu	
385 390 395 400	
cta gag aag aac tta gga cta tcg ccg atc gat gtg gag gca tct aga	1248
Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg	
405 410 415	
tca acg tta cat aga ttt ggg aat act tca tct agc tca att tgg tat	1296
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr	
420 425 430	
gaa tta gca tac ata gag gca aag gga aga atg aag aaa ggg aat aaa	1344
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys	
435 440 445	
gct tgg cag att gct tta gga tca ggg ttt aag tgt aat agt gct gtt	1392
Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val	
450 455 460	
tgg gtg gct cta cgc aat gtc aag gca tcg gca aat agt cct tgg caa	1440
Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln	
465 470 475 480	
cat tgc atc gat aga tat ccg gtt aaa att gat tct gat ttg tca aag	1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys	
485 490 495	
tca aag act cat gtc caa aac ggt cgg tcc taa	1521
Ser Lys Thr His Val Gln Asn Gly Arg Ser	
500 505	

<210> 28
 <211> 506
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 5' 176 amino acids from B. napus elongase KCS (SEQ
 ID NO:4) and 3' 330 amino acids from A. thaliana
 FAE1 (SEQ ID NO:2); designated Bn176

<400> 28

Met Thr Ser Ile Asn Val Lys Leu Leu Tyr His Tyr Val Ile Thr Asn
 1 5 10 15
 Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys
 20 25 30
 Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr
 35 40 45
 Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val
 50 55 60
 Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu
 65 70 75 80
 Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile
 85 90 95
 Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser
 100 105 110
 Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys
 115 120 125
 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly
 130 135 140
 Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu
 145 150 155 160
 Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr
 165 170 175
 Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met
 180 185 190
 Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
 195 200 205
 Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
 210 215 220
 Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
 225 230 235 240
 Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Gly
 245 250 255
 Ile Tyr Ala Gly Glu Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
 260 265 270
 Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Ser Gly Asp Arg
 275 280 285
 Arg Arg Ser Lys Tyr Lys Leu Val His Thr Val Arg Thr His Thr Gly
 290 295 300
 Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Glu Asp Asp Glu Ser
 305 310 315 320
 Gly Lys Ile Gly Val Cys Leu Ser Lys Asp Ile Thr Asn Val Ala Gly
 325 330 335
 Thr Thr Leu Thr Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
 340 345 350
 Leu Ser Glu Lys Phe Leu Phe Phe Ala Thr Phe Val Ala Lys Lys Leu
 355 360 365
 Leu Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
 370 375 380
 Val Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu
 385 390 395 400
 Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr
 420 425 430
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys

435	440	445
Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val		
450	455	460
Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln		
465	470	475
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys		480
485	490	495
Ser Lys Thr His Val Gln Asn Gly Arg Ser		
500	505	

<210> 29

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 1197 bp from A. thaliana FAE1 (SEQ ID NO:1) and
3' 324 bp from B. napus elongase KCS (SEQ ID
NO:3); designated At399

<221> CDS

<222> (1) ... (1518)

<400> 29

atg acg tcc gtt aac gtt aag ctc ctt tac cgt tac gtc tta acc aac	48
Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn	
1 5 10 15	

ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa	96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys	
20 25 30	

gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc	144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu	
35 40 45	

caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc	192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe	
50 55 60	

ggt ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt	240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val	
65 70 75 80	

gac tac tcg tgt tac ctt cca cca ccg cat ctc aaa gtt agt gtc tct	288
Asp Tyr Ser Cys Tyr Leu Pro Pro His Leu Lys Val Ser Val Ser	
85 90 95	

aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca	336
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser	
100 105 110	

cgg aac gtg gca tgt gat gat ccg tcc tcg ctc gat ttc ctg agg aag	384
Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys	
115 120 125	

att caa gag cgt tca ggt cta ggt gat gag acg tac agt cct gag gga Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly 130 135 140	432
ctc att cac gta cca ccg cg aag act ttt gca gcg tca cgt gaa gag Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu 145 150 155 160	480
aca gag aag gtt atc atc ggt gcg ctc gaa aat cta ttc gag aac acc Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Glu Asn Thr 165 170 175	528
aaa gtt aac cct aga gag att ggt ata ctt gtg gtg aac tca agc atg Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met 180 185 190	576
ttt aat cca act cct tcg cta tcc gct atg gtc gtt aat act ttc aag Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys 195 200 205	624
ctc cga agc aac atc aaa agc ttt aat cta gga gga atg ggt tgt agt Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser 210 215 220	672
gct ggt gtt att gcc att gat ttg gct aaa gac ttg ttg cat gtt cat Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His 225 230 235 240	720
aaa aac act tat gct ctt gtg gtg agc act gag aac atc aca caa ggc Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Gly 245 250 255	768
att tat gct gga gaa aat aga tca atg atg gtt agc aat tgc ttg ttt Ile Tyr Ala Gly Glu Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe 260 265 270	816
cgt gtt ggt ggg gcc gcg att ttg ctc tct aac aag tcg gga gac cg Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Ser Gly Asp Arg 275 280 285	864
aga cgg tcc aag tac aag cta gtt cac acg gtc cga acg cat act gga Arg Arg Ser Lys Tyr Lys Leu Val His Thr Val Arg Thr His Thr Gly 290 295 300	912
gct gat gac aag tct ttt cga tgt gtg caa caa gaa gac gat gag agc Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Glu Asp Asp Glu Ser 305 310 315 320	960
ggc aaa atc gga gtt tgt ctg tca aag gac ata acc aat gtt gcg ggg Gly Lys Ile Gly Val Cys Leu Ser Lys Asp Ile Thr Asn Val Ala Gly 325 330 335	1008
aca aca ctt acg aaa aat ata gca aca ttg ggt ccg ttg att ctt cct Thr Thr Leu Thr Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro 340 345 350	1056

tta agc gaa aag ttt ctt ttt ttc gct acc ttc gtc gcc aag aaa ctt		1104	
Leu Ser Glu Lys Phe Leu Phe Phe Ala Thr Phe Val Ala Lys Lys Leu			
355	360	365	
ct a aag gat aaa atc aag cat tac tat gtt ccg gat ttc aag ctt gct		1152	
Leu Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala			
370	375	380	
gtt gac cat ttc tgt att cat gcc gga ggc aga gcc gtg atc gat gtg		1200	
Val Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val			
385	390	395	400
ct a gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga		1248	
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg			
405	410	415	
tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat		1296	
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr			
420	425	430	
gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa		1344	
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys			
435	440	445	
gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt		1392	
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val			
450	455	460	
tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa		1440	
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu			
465	470	475	480
cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag		1488	
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys			
485	490	495	
tca gag act cgt gtc cma aac ggt cg g tcc taa		1521	
Ser Glu Thr Arg Val Xaa Asn Gly Arg Ser			
500	505		

<210> 30
 <211> 506
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 5' 399 amino acids from A. thaliana FAE1 (SEQ ID
 NO:2) and 3' 107 amino acids from B. napus
 elongase KCS (SEQ ID NO:4); designated At399

<221> VARIANT
 <222> (0)...(0)
 <223> Xaa = Pro or Gln

<400> 30

Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
 1 5 10 15
 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
 20 25 30
 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
 35 40 45
 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
 50 55 60
 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
 65 70 75 80
 Asp Tyr Ser Cys Tyr Leu Pro Pro His Leu Lys Val Ser Val Ser
 85 90 95
 Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser
 100 105 110
 Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys
 115 120 125
 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly
 130 135 140
 Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu
 145 150 155 160
 Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Glu Asn Thr
 165 170 175
 Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met
 180 185 190
 Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
 195 200 205
 Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
 210 215 220
 Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
 225 230 235 240
 Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Gly
 245 250 255
 Ile Tyr Ala Gly Glu Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
 260 265 270
 Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Ser Gly Asp Arg
 275 280 285
 Arg Arg Ser Lys Tyr Lys Leu Val His Thr Val Arg Thr His Thr Gly
 290 295 300
 Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Glu Asp Asp Glu Ser
 305 310 315 320
 Gly Lys Ile Gly Val Cys Leu Ser Lys Asp Ile Thr Asn Val Ala Gly
 325 330 335
 Thr Thr Leu Thr Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
 340 345 350
 Leu Ser Glu Lys Phe Leu Phe Phe Ala Thr Phe Val Ala Lys Lys Leu
 355 360 365
 Leu Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
 370 375 380
 Val Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
 385 390 395 400
 Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
 420 425 430
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445

Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
 465 470 475 480
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
 485 490 495
 Ser Glu Thr Arg Val Xaa Asn Gly Arg Ser
 500 505

<210> 31
 <211> 1521
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 5' 1197 bp from *B. napus* elongase KCS (SEQ ID NO:3) and 3' 324 bp from *A. thaliana* FAE1 (SEQ ID NO:1); designated Bn399

<221> CDS
 <222> (1)...(1518)

<400> 31
 atg acg tcc att aac gtt aag ctc ctt tac cat tac gtc ata acc aac 48
 Met Thr Ser Ile Asn Val Lys Leu Leu Tyr His Tyr Val Ile Thr Asn
 1 5 10 15
 ctt ttc aac ctt tgc ttc ttt ccg tta acg gcg atc gtc gcc gga aaa 96
 Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys
 20 25 30
 gcc tat cgg ctt acc ata gac gat ctt cac cac tta tac tat tcc tat 144
 Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr
 35 40 45
 ctc caa cac aac ctc ata acc atc gct cca ctc ttt gcc ttc acc gtt 192
 Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val
 50 55 60
 ttc ggt tcg gtt ctc tac atc gca acc cgg ccc aaa ccg gtt tac ctc 240
 Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu
 65 70 75 80
 gtt gag tac tca tgc tac ctt cca cca acg cat tgt aga tca agt atc 288
 Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile
 85 90 95
 tcc aag gtc atg gat atc ttt tat caa gta aga aaa gct gat cct tct 336
 Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser
 100 105 110
 cgg aac ggc acg tgc gat gac tcg tcg tgg ctt gac ttc ttg agg aag 384
 Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys
 115 120 125
 att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg 432

Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly			
130	135	140	
ctg ctt cag gtc cct ccc cg ^g aag act ttt g ^c g ^c g ^c cgt gaa gag			480
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu			
145	150	155	160
acg gag caa gtt atc att ggt g ^c g ^c aat cta ttc aag aac acc			528
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr			
165	170	175	
aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg			576
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met			
180	185	190	
ttt aat cca act cca tcg ctc tcc g ^c g ^c atg gtc gtt aac act ttc aag			624
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys			
195	200	205	
ctc cga agc aac gta aga agc ttt aac ctt ggt g ^c atg g ^c g ^c tgt agt			672
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser			
210	215	220	
gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat			720
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His			
225	230	235	240
aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac			768
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn			
245	250	255	
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc			816
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe			
260	265	270	
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt			864
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg			
275	280	285	
aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga			912
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly			
290	295	300	
gct gac ggc aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac			960
Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn			
305	310	315	320
ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt			1008
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly			
325	330	335	
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg			1056
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro			
340	345	350	
tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt			1104

Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu	355	360	365	
ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct				1152
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala	370	375	380	
att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg atc gat gag				1200
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu	385	390	395	400
cta gag aag aac tta gga cta tcg ccg atc gat gtg gag gca tct aga				1248
Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg	405	410	415	
tca acg tta cat aga ttt ggg aat act tca tct agc tca att tgg tat				1296
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr	420	425	430	
gaa tta gca tac ata gag gca aag gga aga atg aag aaa ggg aat aaa				1344
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys	435	440	445	
gct tgg cag att gct tta gga tca ggg ttt aag tgt aat agt gcg gtt				1392
Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val	450	455	460	
tgg gtg gct cta cgc aat gtc aag gca tcg gca aat agt cct tgg caa				1440
Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln	465	470	475	480
cat tgc atc gat aga tat ccg gtt aaa att gat tct gat ttg tca aag				1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys	485	490	495	
tca aag act cat gtc caa aac ggt cgg tcc taa				1521
Ser Lys Thr His Val Gln Asn Gly Arg Ser	500	505		

<210> 32
<211> 506
<212> PRT
<213> Artificial Sequence

<220>
<223> 5' 399 amino acids from *B. napus* elongase KCS (SEQ
ID NO:3) and 3' 107 amino acids from *A. thaliana*
FAE1 (SEQ ID NO:1); designated Bn399

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<400> 32
Met Thr Ser Ile Asn Val Lys Leu Leu Tyr His Tyr Val Ile Thr Asn
      1           5           10          15
Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys
      20          25          30
Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr

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35	40	45
Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val		
50 55 60		
Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu		
65 70 75 80		
Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile		
85 90 95		
Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser		
100 105 110		
Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys		
115 120 125		
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly		
130 135 140		
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu		
145 150 155 160		
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr		
165 170 175		
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met		
180 185 190		
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys		
195 200 205		
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser		
210 215 220		
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His		
225 230 235 240		
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn		
245 250 255		
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe		
260 265 270		
Arg Val Gly Gly Ala Ala Ile Leu Ser Asn Lys Pro Gly Asp Arg		
275 280 285		
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly		
290 295 300		
Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn		
305 310 315 320		
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly		
325 330 335		
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro		
340 345 350		
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu		
355 360 365		
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala		
370 375 380		
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu		
385 390 395 400		
Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg		
405 410 415		
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr		
420 425 430		
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys		
435 440 445		
Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val		
450 455 460		
Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln		
465 470 475 480		
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys		

485	490	495
Ser Lys Thr His Val Gln Asn Gly Arg Ser		
500	505	
<210> 33		
<211> 1524		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> 1524 bp from B. napus elongase KCS (SEQ ID NO:3)		
having a mutation at position 920; designated Bn		
G307D; hypothetical		
<221> CDS		
<222> (1) . . . (1518)		
<400> 33		
atg acg tcc att aac gta aag ctc ctt tac cat tac gtc ata acc aac		48
Met Thr Ser Ile Asn Val Lys Leu Leu Tyr His Tyr Val Ile Thr Asn		
1	5	10
		15
ctt ttc aac ctt tgc ttc ttt ccg tta acg gcg atc gtc gcc gga aaa		96
Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys		
20	25	30
gcc tat cgg ctt acc ata gac gat ctt cac cac tta tac tat tcc tat		144
Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr		
35	40	45
ctc caa cac aac ctc ata acc atc gct cca ctc ttt gcc ttc acc gtt		192
Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val		
50	55	60
ttc ggt tcg gtt ctc tac atc gca acc cgg ccc aaa ccg gtt tac ctc		240
Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu		
65	70	75
		80
gtt gag tac tca tgc tac ctt cca cca acg cat tgt aga tca agt atc		288
Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile		
85	90	95
tcc aag gtc atg gat atc ttt tat caa gta aga aaa gct gat cct tct		336
Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser		
100	105	110
cgg aac ggc acg tgc gat gac tcg tcg tgg ctt gac ttc ttg agg aag		384
Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys		
115	120	125
att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg		432
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly		
130	135	140
ctg ctt cag gtc cct ccc cg aag act ttt gcg gcg cgt gaa gag		480
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Arg Glu Glu		

145	150	155	160	
acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc				528
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr				
165	170	175		
aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg				576
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met				
180	185	190		
ttt aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag				624
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys				
195	200	205		
ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt				672
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser				
210	215	220		
gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat				720
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His				
225	230	235	240	
aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac				768
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn				
245	250	255		
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc				816
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe				
260	265	270		
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt				864
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg				
275	280	285		
aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga				912
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly				
290	295	300		
gct gac gac aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac				960
Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn				
305	310	315	320	
ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt				1008
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly				
325	330	335		
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg				1056
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro				
340	345	350		
tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt				1104
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu				
355	360	365		
ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct				1152
Phe Lys Asp Lys Ile Lys His Tyr Val Pro Asp Phe Lys Leu Ala				

370	375	380	
att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val			1200
385	390	395	400
cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg			1248
405	410	415	
tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr			1296
420	425	430	
gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys			1344
435	440	445	
gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val			1392
450	455	460	
tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu			1440
465	470	475	480
cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys			1488
485	490	495	
tca gag act cgt gtc caa aac ggt cggt tcc taataa Ser Glu Thr Arg Val Gln Asn Gly Arg Ser			1524
500	505		

<210> 34
 <211> 506
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 506 amino acids from B. napus elongase KCS (SEQ ID NO:4) having a mutation at residue 307; designated Bn G307D; hypothetical

<400> 34
 Met Thr Ser Ile Asn Val Lys Leu Leu Tyr His Tyr Val Ile Thr Asn
 1 5 10 15
 Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys
 20 25 30
 Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr
 35 40 45
 Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val
 50 55 60
 Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu
 65 70 75 80

Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile
 85 90 95
 Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser
 100 105 110
 Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys
 115 120 125
 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly
 130 135 140
 Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu
 145 150 155 160
 Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr
 165 170 175
 Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met
 180 185 190
 Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
 195 200 205
 Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
 210 215 220
 Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
 225 230 235 240
 Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn
 245 250 255
 Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
 260 265 270
 Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg
 275 280 285
 Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly
 290 295 300
 Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn
 305 310 315 320
 Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly
 325 330 335
 Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
 340 345 350
 Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
 355 360 365
 Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
 370 375 380
 Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
 385 390 395 400
 Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr
 420 425 430
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
 465 470 475 480
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
 485 490 495
 Ser Glu Thr Arg Val Gln Asn Gly Arg Ser
 500 505

<211> 1709
 <212> DNA
 <213> Artificial Sequence

<220>

<223> 1709 bp from A. thaliana FAE1 (SEQ ID NO:1) having
 a mutation at position 275; designated At K92R;
 hypothetical

<221> CDS
 <222> (1) ... (1518)

<400> 35

atg acg tcc gtt aac gtt aag ctc ctt tac cgt tac gtc tta acc aac	48
Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn	
1 5 10 15	

ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa	96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys	
20 25 30	

gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc	144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu	
35 40 45	

caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc	192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe	
50 55 60	

ggt ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt	240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val	
65 70 75 80	

gac tac tcg tgt tac ctt cca cca ccg cat ctc aga gtt agt gtc tct	288
Asp Tyr Ser Cys Tyr Leu Pro Pro His Leu Arg Val Ser Val Ser	
85 90 95	

aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca	336
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser	
100 105 110	

ccg aac gtg gca tgt gat gat ccg tcc tcg ctc gat ttc ctg agg aag	384
Arg Asn Val Ala Cys Asp Asp Ser Ser Leu Asp Phe Leu Arg Lys	
115 120 125	

att caa gag cgt tca ggt cta ggt gat gag acg tac agt cct gag gga	432
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly	
130 135 140	

ctc att cac gta cca ccg cgg aag act ttt gca gcg tca cgt gaa gag	480
Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu	
145 150 155 160	

aca gag aag gtt atc atc ggt gcg ctc gaa aat cta ttc gag aac acc	528
Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Glu Asn Thr	
165 170 175	

aaa gtt aac cct aga gag att ggt ata ctt gtg gtg aac tca agc atg		576	
Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met			
180	185	190	
ttt aat cca act cct tcg cta tcc gct atg gtc gtt aat act ttc aag		624	
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys			
195	200	205	
ctc cga agc aac atc aaa agc ttt aat cta gga gga atg ggt tgt agt		672	
Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser			
210	215	220	
gct ggt gtt att gcc att gat ttg gct aaa gac ttg ttg cat gtt cat		720	
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His			
225	230	235	240
aaa aac act tat gct ctt gtg gtg agc act gag aac atc aca caa ggc		768	
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Gly			
245	250	255	
att tat gct gga gaa aat aga tca atg atg gtt agc aat tgc ttg ttt		816	
Ile Tyr Ala Gly Glu Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe			
260	265	270	
cgt gtt ggt ggg gcc gcg att ttg ctc tct aac aag tcg gga gac cgg		864	
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Ser Gly Asp Arg			
275	280	285	
aga cggtcc aag tac aag cta gtt cac acg gtc cga acg cat act gga		912	
Arg Arg Ser Lys Tyr Lys Leu Val His Thr Val Arg Thr His Thr Gly			
290	295	300	
gct gat gac aag tct ttt cga tgt gtg caa caa gaa gac gat gag agc		960	
Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Glu Asp Asp Glu Ser			
305	310	315	320
ggc aaa atc gga gtt tgt ctg tca aag gac ata acc aat gtt gcg ggg		1008	
Gly Lys Ile Gly Val Cys Leu Ser Lys Asp Ile Thr Asn Val Ala Gly			
325	330	335	
aca aca ctt acg aaa aat ata gca aca ttg ggt ccg ttg att ctt cct		1056	
Thr Thr Leu Thr Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro			
340	345	350	
tta agc gaa aag ttt ctt ttt ttc gct acc ttc gtc gcc aag aaa ctt		1104	
Leu Ser Glu Lys Phe Leu Phe Phe Ala Thr Phe Val Ala Lys Lys Leu			
355	360	365	
cta aag gat aaa atc aag cat tac tat gtt ccg gat ttc aag ctt gct		1152	
Leu Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala			
370	375	380	
gtt gac cat ttc tgt att cat gcc gga ggc aga gcc gtg atc gat gag		1200	
Val Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu			
385	390	395	400

cta gag aag aac tta gga cta tcg ccg atc gat gtg gag gca tct aga	1248	
Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg		
405 410 415		
tca acg tta cat aga ttt ggg aat act tca tct agc tca att tgg tat	1296	
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr		
420 425 430		
gaa tta gca tac ata gag gca aag gga aga atg aag aaa ggg aat aaa	1344	
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys		
435 440 445		
gct tgg cag att gct tta gga tca ggg ttt aag tgt aat agt gcg gtt	1392	
Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val		
450 455 460		
tgg gtg gct cta cgc aat gtc aag gca tcg gca aat agt cct tgg caa	1440	
Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln		
465 470 475 480		
cat tgc atc gat aga tat ccg gtt aaa att gat tct gat ttg tca aag	1488	
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys		
485 490 495		
tca aag act cat gtc caa aac ggt cggtcc taatttgatg tatctgagtg	1538	
Ser Lys Thr His Val Gln Asn Gly Arg Ser		
500 505		
ccaacgttta ctttgccttt cctttctttt attgggtatg aatttagatgt ttactaatgt	1598	
tcctctctttt ttcgttataa ataaagaagt tcaattcttc ctatagttc aaacgcgatt	1658	
ttaagcgttt ctat taggt ttacatgaat ttctttaca aaccatcttt t	1709	
<210> 36		
<211> 506		
<212> PRT		
<213> Artificial Sequence		
<220>		
<223> 506 amino acids from A. thaliana FAE1 (SEQ ID NO:2) having a mutation at residue 92; designated At K92R; hypothetical		
<400> 36		
Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn		
1 5 10 15		
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys		
20 25 30		
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu		
35 40 45		
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe		
50 55 60		
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val		
65 70 75 80		
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Arg Val Ser Val Ser		
85 90 95		

Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser
 100 105 110
 Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys
 115 120 125
 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly
 130 135 140
 Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu
 145 150 155 160
 Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Glu Asn Thr
 165 170 175
 Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met
 180 185 190
 Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
 195 200 205
 Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
 210 215 220
 Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
 225 230 235 240
 Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Gly
 245 250 255
 Ile Tyr Ala Gly Glu Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
 260 265 270
 Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Ser Gly Asp Arg
 275 280 285
 Arg Arg Ser Lys Tyr Lys Leu Val His Thr Val Arg Thr His Thr Gly
 290 295 300
 Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Glu Asp Asp Glu Ser
 305 310 315 320
 Gly Lys Ile Gly Val Cys Leu Ser Lys Asp Ile Thr Asn Val Ala Gly
 325 330 335
 Thr Thr Leu Thr Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
 340 345 350
 Leu Ser Glu Lys Phe Leu Phe Phe Ala Thr Phe Val Ala Lys Lys Leu
 355 360 365
 Leu Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
 370 375 380
 Val Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu
 385 390 395 400
 Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
 420 425 430
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445
 Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460
 Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln
 465 470 475 480
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys
 485 490 495
 Ser Lys Thr His Val Gln Asn Gly Arg Ser
 500 505

<210> 37

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 762 bp from A. thaliana FAE1 (SEQ ID NO:1) and
3' 759 bp from B. napus elongase KCS (SEQ ID NO:3)
and having a mutation at position 920; designated
At254 G307D; hypothetical

<221> CDS

<222> (1) ... (1518)

<400> 37

atg acg tcc gtt aac gtt aag ctc ctt tac cgt tac gtc tta acc aac	48
Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn	
1 5 10 15	
ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa	96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys	
20 25 30	
gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc	144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu	
35 40 45	
caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc	192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe	
50 55 60	
ggg ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt	240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val	
65 70 75 80	
gac tac tcg tgt tac ctt cca cca ccg cat ctc aaa gtt agt gtc tct	288
Asp Tyr Ser Cys Tyr Leu Pro Pro His Leu Lys Val Ser Val Ser	
85 90 95	
aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca	336
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser	
100 105 110	
ccg aac gtg gca tgt gat gat ccg tcc tcg ctc gat ttc ctg agg aag	384
Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys	
115 120 125	
att caa gag cgt tca ggt cta ggt gat gag acg tac agt cct gag gga	432
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly	
130 135 140	
ctc att cac gta cca ccg cgg aag act ttt gca gcg tca cgt gaa gag	480
Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu	
145 150 155 160	
aca gag aag gtt atc atc ggt gcg ctc gaa aat cta ttc gag aac acc	528
Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Glu Asn Thr	
165 170 175	

aaa gtt aac cct aga gag att ggt ata ctt gtg gtg aac tca agc atg Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met 180 185 190	576
ttt aat cca act cct tcg cta tcc gct atg gtc gtt aat act ttc aag Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys 195 200 205	624
ctc cga agc aac atc aaa agc ttt aat cta gga gga atg ggt tgt agt Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser 210 215 220	672
gct ggt gtt att gcc att gat ttg gct aaa gac ttg ttg cat gtt cat Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His 225 230 235 240	720
aaa aac act tat gct ctc gtg gtg agc aca gag aac atc act tat aac Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn 245 250 255	768
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe 260 265 270	816
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg 275 280 285	864
aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly 290 295 300	912
gct gac gac aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn 305 310 315 320	960
ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly 325 330 335	1008
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro 340 345 350	1056
tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu 355 360 365	1104
ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala 370 375 380	1152
att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val 385 390 395 400	1200

cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga	1248
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg	
405 410 415	
tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat	1296
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr	
420 425 430	
gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa	1344
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys	
435 440 445	
gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt	1392
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val	
450 455 460	
tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa	1440
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu	
465 470 475 480	
cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag	1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys	
485 490 495	
tca gag act cgt gtc caa aac ggt cggt tcc taa	1521
Ser Glu Thr Arg Val Gln Asn Gly Arg Ser	
500 505	

<210> 38
 <211> 506
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 5' 254 amino acids from A. thaliana FAE1 (SEQ ID NO:2) and 3' 252 amino acids from B. napus elongase KCS (SEQ ID NO:4) having a mutation at residue 307; designated At254 G307D; hypothetical

<400> 38
 Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
 1 5 10 15
 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
 20 25 30
 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
 35 40 45
 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
 50 55 60
 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
 65 70 75 80
 Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser
 85 90 95
 Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser
 100 105 110
 Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys

115	120	125	
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly			
130	135	140	
Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu			
145	150	155	160
Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Glu Asn Thr			
165	170	175	
Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met			
180	185	190	
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys			
195	200	205	
Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser			
210	215	220	
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His			
225	230	235	240
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn			
245	250	255	
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe			
260	265	270	
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg			
275	280	285	
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly			
290	295	300	
Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn			
305	310	315	320
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly			
325	330	335	
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro			
340	345	350	
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu			
355	360	365	
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala			
370	375	380	
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val			
385	390	395	400
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg			
405	410	415	
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr			
420	425	430	
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys			
435	440	445	
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val			
450	455	460	
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu			
465	470	475	480
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys			
485	490	495	
Ser Glu Thr Arg Val Gln Asn Gly Arg Ser			
500	505		

<210> 39

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 519 bp from A. thaliana FAE1 (SEQ ID NO:1) and
 3' 1002 bp from B. napus elongase KCS (SEQ ID
 NO:3) and having a mutation at position 920;
 designated At173 G307D

<221> CDS
 <222> (1) ... (1518)

<400> 39

atg acg tcc gtt aac gtt aag ctc ctt tac cgt tac gtc tta acc aac	48
Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn	
1 5 10 15	
ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa	96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys	
20 25 30	
gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc	144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu	
35 40 45	
caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc	192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe	
50 55 60	
ggt ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt	240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val	
65 70 75 80	
gac tac tcg tgt tac ctt cca cca ccg cat ctc aaa gtt agt gtc tct	288
Asp Tyr Ser Cys Tyr Leu Pro Pro His Leu Lys Val Ser Val Ser	
85 90 95	
aaa gtc atg gat att ttc taccaa ata aga aaa gct gat act tct tca	336
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser	
100 105 110	
ccg aac gtg gca tgt gat ccg tcc tcg ctc gat ttc ctg agg aag	384
Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys	
115 120 125	
att caa gag cgt tca ggt cta ggt gat gag acg tac agt cct gag gga	432
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly	
130 135 140	
ctc att cac gta cca ccg ccg aag act ttt gca gcg tca cgt gaa gag	480
Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu	
145 150 155 160	
aca gag aag gtt atc atc ggt gcg ctc gaa aat cta ttc aag aac acc	528
Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr	
165 170 175	
aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg	576
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met	
180 185 190	

ttt aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag			624
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys			
195	200	205	
ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt			672
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser			
210	215	220	
gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat			720
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His			
225	230	235	240
aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac			768
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn			
245	250	255	
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc			816
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe			
260	265	270	
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt			864
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg			
275	280	285	
aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga			912
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly			
290	295	300	
gct gac gac aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac			960
Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn			
305	310	315	320
ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt			1008
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly			
325	330	335	
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg			1056
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro			
340	345	350	
tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt			1104
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu			
355	360	365	
ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct			1152
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala			
370	375	380	
att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg			1200
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val			
385	390	395	400
cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga			1248
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg			
405	410	415	

tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat	1296		
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr			
420	425	430	
gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa	1344		
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys			
435	440	445	
gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt	1392		
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val			
450	455	460	
tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa	1440		
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu			
465	470	475	480
cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag	1488		
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys			
485	490	495	
tca gag act cgt gtc caa aac ggt cg ^g tcc taa	1521		
Ser Glu Thr Arg Val Gln Asn Gly Arg Ser			
500	505		

<210> 40
 <211> 506
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 5' 173 amino acids from A. thaliana FAE1 (SEQ ID
 NO:2) and 3' 333 amino acids from B. napus
 elongase KCS (SEQ ID NO:4) having a mutation at
 residue 307; designated At173 G307D; hypothetical

<400> 40
 Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
 1 5 10 15
 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
 20 25 30
 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
 35 40 45
 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
 50 55 60
 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
 65 70 75 80
 Asp Tyr Ser Cys Tyr Leu Pro Pro His Leu Lys Val Ser Val Ser
 85 90 95
 Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser
 100 105 110
 Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys
 115 120 125
 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly
 130 135 140

Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu
 145 150 155 160
 Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr
 165 170 175
 Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met
 180 185 190
 Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
 195 200 205
 Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
 210 215 220
 Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
 225 230 235 240
 Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn
 245 250 255
 Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
 260 265 270
 Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg
 275 280 285
 Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly
 290 295 300
 Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn
 305 310 315 320
 Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly
 325 330 335
 Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
 340 345 350
 Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
 355 360 365
 Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
 370 375 380
 Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
 385 390 395 400
 Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
 420 425 430
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
 465 470 475 480
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
 485 490 495
 Ser Glu Thr Arg Val Gln Asn Gly Arg Ser
 500 505

<210> 41
 <211> 1521
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 5' 1197 bp from B. napus elongase KCS (SEQ ID
 NO:3) and 3' 324 bp from A. thaliana FAE1 (SEQ ID
 NO:1) and having a mutation at nucleotide position

920; designated Bn399 G307D; hypothetical

<221> CDS

<222> (1) ... (1518)

<400> 41

atg acg tcc att aac gtt aag ctc ctt tac cat tac gtc ata acc aac 48
 Met Thr Ser Ile Asn Val Lys Leu Leu Tyr His Tyr Val Ile Thr Asn
 1 5 10 15

ctt ttc aac ctt tgc ttc ttt ccg tta acg gcg atc gtc gcc gga aaa 96
 Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys
 20 25 30

gcc tat cgg ctt acc ata gac gat ctt cac cac tta tac tat tcc tat 144
 Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr
 35 40 45

ctc caa cac aac ctc ata acc atc gct cca ctc ttt gcc ttc acc gtt 192
 Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val
 50 55 60

ttc ggt tcg gtt ctc tac atc gca acc cgg ccc aaa ccg gtt tac ctc 240
 Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu
 65 70 75 80

gtt gag tac tca tgc tac ctt cca cca acg cat tgt aga tca agt atc 288
 Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile
 85 90 95

tcc aag gtc atg gat atc ttt tat caa gta aga aaa gct gat cct tct 336
 Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser
 100 105 110

cgg aac ggc acg tgc gat gac tcg tcg tgg ctt gac ttc ttg agg aag 384
 Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys
 115 120 125

att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg 432
 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly
 130 135 140

ctg ctt cag gtc cct ccc cgg aag act ttt gcg gcg gcg cgt gaa gag 480
 Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu
 145 150 155 160

acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc 528
 Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr
 165 170 175

aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg 576
 Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met
 180 185 190

ttt aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag 624
 Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys

195	200	205			
ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser	210	215	220	672	
gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His	225	230	235	240	720
aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn	245	250	255		768
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe	260	265	270		816
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg	275	280	285		864
aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly	290	295	300		912
gct gac gac aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn	305	310	315	320	960
ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly	325	330	335		1008
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro	340	345	350		1056
tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu	355	360	365		1104
ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala	370	375	380		1152
att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg atc gat gag Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu	385	390	395	400	1200
cta gag aag aac tta gga cta tcg ccg atc gat gtg gag gca tct aga Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg	405	410	415		1248
tca acg tta cat aga ttt ggg aat act tca tct agc tca att tgg tat Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr					1296

420	425	430	
gaa tta gca tac ata gag gca aag gga aga atg aag aaa ggg aat aaa			1344
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys			
435	440	445	
gct tgg cag att gct tta gga tca ggg ttt aag tgt aat agt gcg gtt			1392
Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val			
450	455	460	
tgg gtg gct cta cgc aat gtc aag gca tcg gca aat agt cct tgg caa			1440
Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln			
465	470	475	480
cat tgc atc gat aga tat ccg gtt aaa att gat tct gat ttg tca aag			1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys			
485	490		495
tca aag act cat gtc caa aac ggt cggt tcc taa			1521
Ser Lys Thr His Val Gln Asn Gly Arg Ser			
500	505		

<210> 42
 <211> 506
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 5' 399 amino acids from B. napus elongase KCS (SEQ ID NO:3) and 3' 107 amino acids from A. thaliana FAE1 (SEQ ID NO:1) having a mutation at residue 306; designated Bn399 G307D; hypothetical

<400> 42
 Met Thr Ser Ile Asn Val Lys Leu Leu Tyr His Tyr Val Ile Thr Asn
 1 5 10 15
 Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys
 20 25 30
 Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr
 35 40 45
 Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val
 50 55 60
 Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu
 65 70 75 80
 Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile
 85 90 95
 Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser
 100 105 110
 Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys
 115 120 125
 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly
 130 135 140
 Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu
 145 150 155 160
 Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr

165	170	175	
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met			
180	185	190	
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys			
195	200	205	
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser			
210	215	220	
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His			
225	230	235	
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn			
245	250	255	
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe			
260	265	270	
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg			
275	280	285	
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly			
290	295	300	
Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn			
305	310	315	320
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly			
325	330	335	
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro			
340	345	350	
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu			
355	360	365	
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala			
370	375	380	
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu			
385	390	395	400
Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg			
405	410	415	
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr			
420	425	430	
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys			
435	440	445	
Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val			
450	455	460	
Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln			
465	470	475	480
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys			
485	490	495	
Ser Lys Thr His Val Gln Asn Gly Arg Ser			
500	505		

<210> 43

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> primer for PCR

<400> 43

gcgctcgaaa atctattcaa gaaca

<210> 44

<211> 33		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> primer for PCR		
<400> 44		
gttcttgaat agatttcga gcgcaccgat gat		33
<210> 45		
<211> 28		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> primer for PCR		
<400> 45		
cggaacggca cgtgtatga ttcgtcct		28
<210> 46		
<211> 28		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> primer for PCR		
<400> 46		
aggacggatc atcacacgca acgttccg		28
<210> 47		
<211> 23		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> primer for PCR		
<400> 47		
cccaaaccgg tttacctcgt tga		23
<210> 48		
<211> 23		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> primer for PCR		
<400> 48		
tcaacgaggt aaaccggatt ggg		23
<210> 49		
<211> 27		

<212> DNA		
<213> Artificial Sequence		
<220>		
<223> primer for PCR		
<400> 49		
ccgcattgca gagtttgtt ctctaaa	27	
<210> 50		
<211> 27		
<212> DNA		
<213> Artificial Sequence		
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<223> primer for PCR		
<400> 50		
tttagagaca ctaactctgc aatgcgg	27	
<210> 51		
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<212> DNA		
<213> Artificial Sequence		
<220>		
<223> primer for PCR		
<400> 51		
ccaccggatc tcagagttt tagtctct	27	
<210> 52		
<211> 27		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> primer for PCR		
<400> 52		
agagacacta actctgagat gcgggtgg	27	
<210> 53		
<211> 33		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> primer for PCR		
<400> 53		
ggggatccat gacgtccgtt aacgttaagc tcc	33	
<210> 54		
<211> 31		
<212> DNA		

<213> Artificial Sequence

<220>

<223> primer for PCR

<400> 54

ccgaattctt aggaccgacc gttttggaca c

31

<210> 55

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> primer for PCR

<400> 55

ggggatccat gacgtccatt aacgtaaagc tcc

33

<210> 56

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> primer for PCR

<400> 56

ccgaattctt aggaccgacc gttttggaca tgagtctt

38